

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:36:04 ; Search time 32.6424 Seconds  
(without alignments)  
1630.025 Million cell updates/sec

Title: US-09-745-792A-11  
Perfect score: 2947  
Sequence: 1 MRAPGPALRPPLPLLLLL.....NETYLMQFMENGLYQVMEN 553

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268.5	9.1	349	2 JC6311	interferon recepto
2	253.5	8.6	325	2 A47003	cytokine receptor
3	225	7.6	575	2 A49667	interleukin-10 rec
4	222.5	7.6	590	2 A45283	interferon alpha/b
5	199.5	6.8	560	2 S27387	interferon alpha r
6	198.5	6.7	489	2 A31555	interferon gamma r
7	198.5	6.7	578	2 I56215	interleukin-10 rec
8	198	6.7	557	2 A32694	interferon alpha/b
9	192.5	6.5	477	2 A34368	interferon gamma r
10	176.5	6.0	332	2 A49347	interferon gamma r
11	167	5.7	292	1 KFRB3	tissue factor prec
12	167	5.7	337	2 I38500	interferon gamma r
13	156	5.3	292	1 KFB03	tissue factor prec
14	156	5.3	295	1 KFH03	tissue factor prec
15	148.5	5.0	515	2 I39073	interferon alpha-b
16	147.5	5.0	917	2 I49699	glycoprotein i30 -
17	143	4.9	294	1 KPM53	tissue factor prec
18	142.5	4.8	896	2 I56563	interleukin-3 rece
19	131	4.4	896	1 A35782	cytokine receptor
20	128.5	4.4	1375	2 T13822	frizzled gene prot
21	128.5	4.4	1526	2 T13823	frizzled gene prot
22	127.5	4.3	3924	2 S37431	ankyrin 2, neuona
23	126.5	4.3	918	2 A36337	membrane glycoprot
24	125.5	4.3	2215	2 T00348	lxl1 protein - mou
25	125	4.2	537	2 B46535	interleukin 2 rece
26	124.5	4.2	2477	2 S14428	fibronectin precur
27	124	4.2	331	2 A54295	interferon alpha/b
28	124	4.2	331	2 S59501	interferon recepto
29	120.5	4.1	1651	2 T14160	transmembrane rece

30 120 4.1 918 2 A44257 interleukin-6 sign  
31 118.5 4.0 26926 1 I38344 titin, cardiac mus  
32 117.5 4.0 1222 2 C88504 protein B0361.3 [i  
33 116 3.9 2029 1 TDFELK protein-tyrosine-p  
34 115.5 3.9 1612 2 T30805 dutti protein - mo  
35 114.5 3.9 1912 2 A56178 protein-tyrosine-p  
36 114 3.9 776 2 A46583 neuroendocrine-spe  
37 114 3.9 878 1 A40091 interleukin-3 rece  
38 114 3.9 2302 2 T14328 protein-tyrosine-p  
39 114 3.9 2957 2 T33152 hypothetical prote  
40 113 3.8 976 2 A36355 protein-tyrosine k  
41 112 3.8 354 2 T24873 hypothetical prote  
42 112 3.8 536 2 T27668 hypothetical prote  
43 112 3.8 1162 2 S68438 leptin receptor, s  
44 111.5 3.8 1128 2 A82939 membrane nuclease  
45 110.5 3.7 658 2 S76909 hypothetical prote

## ALIGNMENTS

### RESULT 1

JC6311  
interferon receptor-class II cytokine receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: JC6311  
R:Gibbs, V.C.; Pennica, D.  
Gene 186, 97-101, 1997  
A:Title: CRF2-4: isolation of cDNA clones encoding the human and mouse proteins.  
A:Reference number: JC6311; MUID:97199375; PMID:9047351  
A:Accession: JC6311  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-349 <GIB>  
A:Cross-references: UNIPROT:Q8VHM7; UNIPARC:UPI000017C6DE; GB:U53696

Query Match 9.1%; Score 268.5; DB 2; Length 349;  
Best Local Similarity 27.3%; Pred. No. 7.5e-12;  
Matches 98; Conservative 53; Mismatches 157; Indels 51; Gaps 15;

QY 31 PCVSGGL-----PKPANIITFLSINMKNVLQWTPPEGLQGVKVTYTYQYFIYGQ 78  
Db 3 PCVAGMLGGFLLPALGMIPPPPEKVRMNSVFNILQWEVP-APPKTNLFTAQYESYRS 61  
QY 79 KWLKSECRINIRTYCDLSAETSDEHYQYAKVIMWTKCKSWAESGFYFPLETQIG 138  
Db 62 ---FQDHCKRTASTQCDFS-HLSKY-GDYTVRVRRAELADEHSEWV-NVTFPCPVEDTIIG 114  
QY 139 PPEVALTTDEKSSISVLTAPKWKRNPEDLPSVSMQIYSLNLYNSVLTNKSNTWSQCV 198  
Db 115 PPEMQIESLABSLRFSAPQ-IENEPETW--TLKNYDSWAYRVQYWKNGTNEKFOVS 171  
QY 199 THTLVLTLWLEPNTLYCVHVESFVPGPPRAQPSKOCARTLKQSEFEKAKIFWYVLP 258  
Db 172 PYDSEVRLNLEPWTTCIQVQGLLDQNTGESEFICERTGND---EITPSMIVAILI 228  
QY 259 ISITVLFVSVMGYSIYRIHVGEKH-----PANLIIYGNFEFDKRF----FVPAEK 306  
Db 229 VSVLVVFLFLGCFVVLWLIYKTKHTFRSGTSLPQHLKEFLGHPHHSTFLLSFPFPEE 288  
QY 307 IVTNFTLNI-----SDSKISHQDMSLLGKSSVS-----SLNDPQPSGNLRPQRESEV 357  
Db 289 AEV-FDKLSIISESESGKQSPEDNCASEPPSPDGPRLSKDEAPS----PPHDDPKL 342

### RESULT 2

A47003  
cytokine receptor family class II protein CRF2-4 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C:Accession: A47003; G01418  
R:Luftalla, G.; Gardiner, K.; Uze, G.

Genomics 16, 366-373, 1993  
A;Title: A new member of the cytokine receptor gene family maps on chromosome 21 at less  
A;Reference number: A47003; MUID:93300510; PMID:8314576  
A;Accession: A47003  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-325 <LUT>  
A;Cross-references: UNIPROT:Q08334; UNIPARC:UPI0000048F14; GB:Z17227; NID:g3933378; PIDN:  
R;Lutfalla, G.  
submitted to the EMBL Data Library, April 1994  
A;Reference number: G06935  
A;Accession: G01418  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-123, 'D', 125-268, 'VGRME', <LU2>  
A;Cross-references: UNIPARC:UPI000016A09D; EMBL:U08988; NID:g571295; PID:g571296  
C;Genetics:  
A;Gene: GDB:CRFB4; CRF2-4  
A;Cross-references: GDB:138168; OMIM:1123889  
A;Map position: 21q; 21q22.1-21q22.2  
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1  
C;Keywords: transmembrane protein

Query Match 8.6%; Score 253.5; DB 2; Length 325;  
Best Local Similarity 25.1%; Pred. No. 8.2e-11;  
Matches 84; Conservative 58; Mismatches 141; Indels 51; Gaps 12;

QY 35 GGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYVQYFIYQKKWLKSECRNINRTY 94  
Db 19 GMVPPENVMNSVNFKNILQWSEPAFAG-NLTFQAQVLSYR-----IFQDKMNTLTLE 73

QY 95 CDLSAETSDYEHQYAKVAKIWMGTCKSKWAESGRFYFPFLETOIGPPEVALTTDEKSI 154  
Db 74 CDFSSLSKYGDHT--LRVRAEFADEHSDWNI--TFCEVDVTIIGPGMQVEVLADSLHR 130

QY 155 LTAP-----EKWRNPEDLPVSMQOIYSNLKNVSLNKTNSRTWSQCQVNTHTLVLTWL 208  
Db 131 FLAPKIKENEYETV-----TMKNVNSWTNVQVWKNGTDEKFIQTPQYDFEVLRL 181

QY 209 EPNLTLCVHVSEVPVPPRAQSEKQCATLKQDSEFKAKIIFWVY---LPISITVFL 265  
Db 182 EPMTTYCVQVGRPLDPRNKAQSEVPCQTHDET-----VPSMWAVILMASVFMVC 235

QY 266 FSVWG-----YSYRVIHVGEKHPANLILYGNFDPKRFVPAEKIVINFIPLNIS 317  
Db 236 LALLGCFSLWCYKTKYAFSPRNSLPQHL-----KEFLGHPHNTLLFPFSPFLS 286

QY 318 DSKISHQDMSLLGKSDVSSLNDPQPSGNLRPP 351  
Db 287 DENDV-FDKLSVIAEDSE-SGKQNPQDSCSLGTP 318

RESULT 3  
A49667  
interleukin-10 receptor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: A49667  
R;Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.  
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993  
A;Title: A receptor for interleukin 10 is related to interferon receptors.  
A;Reference number: A49667; MUID:94068585; PMID:8248239  
A;Accession: A49667  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-575 <RES>  
A;Cross-references: UNIPROT:Q61727; UNIPARC:UPI0000023997; GB:L12120; NID:g437615; PIDN:  
C;Genetics:  
A;Gene: IL10R  
A;Superfamily: interleukin-10 receptor IL10R  
C;Keywords: cytokine receptor

Query Match 7.6%; Score 225; DB 2; Length 575;

Best Local Similarity 22.0%; Pred. No. 2.2e-08;  
Matches 127; Conservative 79; Mismatches 224; Indels 148; Gaps 26;

QY 37 LKPKANITFLSINMKNVLQWTPPEGLQGVKVTYVQYFIYQKKWLKSECRNINRTYCD 96  
Db 26 LPSPSYWFARFFQHLHWKPIPN-QSESTYVEVALKQYGNSTWWDIHCRAQAALSCD 84

QY 97 LSAETSDYEHQ---YVAKVKAIMGTKSKWAESGRFYFPFLETOIGPPEVALTTDEKSI 153  
Db 85 LTTFTLDLYHRSYGYRVARVAVNSQVSNWTTI-----ETRFTVDEVILTVD---SV 133

QY 154 VLTA-----PEKWRNPEDLPV--SMQOIYSNLK-YNVSVLNTKSNRTWSQCVTN 200  
Db 134 TLKAMDGIITGTHPPR----PTITPAGDEYEQFKDLRVYKISIRKFSSELKNAIKRVKQ 189

QY 201 HTLAVLTWLEPNTLYCVHVSEFVPPRRAPQSEKQCATLKQDSSSEFKAKIIFWVVLPI 260  
Db 190 EFTFTLVPIGVKRFCKVAVLPRLIESRINKAEWSEEQCLLTTEQ-----YFTVTNLSILVIS 245

QY 261 ITVFLFSVMGYSIYRIYHVGEKHPANL--ILIYGNFDPKRFVPAEKI-----VINFI 312  
Db 246 MLLFCGILVCLVLQWYI-----RHPGKLTPLVLFKKPHD---FFPANPLCPETPDALHIV 297

QY 313 TLNISDDSKISHQDMSLLGKSDVSSLNDPQPSGNLRPPQEEBEVVKHLGVASHL----- 366  
Db 298 DLEVFPKVSLELRD-SVLHGSTD-----SGFGSGKPSLQTEESQFLLLPGSHPQIQGTL 349

QY 367 -----MEIFCDSEBNTGTSFTQOESLSRITPPD-KTVIEYEV-----DVR----- 406  
Db 350 GKEESPLQATCG--DNTDSGICLQEPGLHSGMPAKQKQOLGYTHQDQDSDVNLVQNSP 407

QY 407 -----TTDICA-----GPEQELSLQBEVSTQGTLLSQAALAVLGPOTLOYSYT 451  
Db 408 GQPKYTQDASALGHVCLLEPKAPEKD---QVMVTFQGYKQTRWKAAGAAGPAECLDEEI 464

QY 452 PQQLDLDPLAQBHTDSEGEPEEPSTTLVDMPQGTGLCIPSLSS---FQDSEGCPESEG 509  
Db 465 PLTDAPDPELGVHLQDD-----LAWPP-----PALAAGYLKQESQGMASA-- 504

QY 510 DGLGEBGLLSLYEPPADPRPGENETLYLMQFMEWGL 547  
Db 505 -----PPGTPSRQNWQLTEEWSL 522

RESULT 4  
A45283  
interferon alpha/beta receptor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 25-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A45283; 148423; 148424; 148425; 148426; 148427; 148428; 148429  
R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogenssen, K.E.  
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992  
A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homospes  
A;Reference number: A45283; MUID:92262522; PMID:1533935  
A;Accession: A45283  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-590 <UZE>  
A;Cross-references: UNIPROT:P33896; UNIPARC:UPI0000027A2F; GB:M89641; NID:g194111; PIDN:  
R;Lutfalla, G.; Uze, G.  
Gene 148, 343-346, 1994  
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-freq  
A;Reference number: 148423; MUID:95047447; PMID:7958966  
A;Accession: 148423  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 118-125 <RES>  
A;Cross-references: UNIPARC:UPI0000000524; EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PI  
A;Accession: 148424  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 127-224 <RE2>

A;Cross-references: UNIPARC:UPI00000000525; EMBL:U06238; NID:g497104; PIDN:AAC01749.1; P  
A;Accession: I48425  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: DNA  
A;Residues: 243-264 <RE3>  
A;Cross-references: UNIPARC:UPI00000000526; EMBL:U06239; NID:g497106; PIDN:AAA65004.1; P  
A;Accession: I48426  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: DNA  
A;Residues: 265-375 <RE4>  
A;Cross-references: UNIPARC:UPI00000000527; EMBL:U06240; NID:g497108; PIDN:AAA65005.1; P  
A;Accession: I48427  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: DNA  
A;Residues: 397-424 <RE5>  
A;Cross-references: UNIPARC:UPI00000000528; EMBL:U06241; NID:g497110; PIDN:AAA65006.1; P  
A;Accession: I48428  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: DNA  
A;Residues: 436-445 <RE6>  
A;Cross-references: UNIPARC:UPI00000000529; EMBL:U06242; NID:g497112; PIDN:AAA65007.1; P  
A;Accession: I48429  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: DNA  
A;Residues: 473-590 <RE7>  
A;Cross-references: UNIPARC:UPI0000000052A; EMBL:U06244; NID:g497114; PIDN:AAA65008.1; P  
C;Genetics:  
A;Gene: IFNAR  
A;Introns: 177/3; 331/1  
C;Keywords: cytokine receptor; transmembrane protein

Query Match 7.6%; Score 222.5; DB 2; Length 590;  
Best Local Similarity 19.1%; Pred. No. 3.5e+08;  
Matches 122; Conservative 96; Mismatches 233; Indels 187; Gaps 24;

Qy	18	LLLLAAPGWRAPVCVSGG--LPKANITFLSINMKVQLQWTPPEGLOGVKVYTYVQYFI	75
Db	10	LVLVAGAPW--VLPSAAGGKLPENIDYIIDNYTLKWSHGSMG-SVTFSAEYRT	66
Qy	76	YGOKKWLKSECRNINITYCDLSAETSDYEHQYKVAIWGTKCSKWAESSGRFPYPLET	135
Db	67	KDEAKWLKVPQCQTTTTTKCEFLSDTNVYIKQFRVRAEGNSTSWNEVDPIFYTA	126
Qy	136	QIGPPEVALTTDEKISVWLTP-----EKWRNPEDLPVSMQOIYSLKYNVSLNTKSN	191
Db	127	HMSPEVLEAEDKAILVHISPPQDGNW-----ALEK--PSFSYTIWQKSSS	175
Qy	192	RTWSQCVTNHTLVLTWLEPNLYICVHVESFVPGPPRAQSPSEKQCARTL-----K	241
Db	176	DKKTINSTYVYEKIPPELLPETTYCLEYKAHPSLKHSNSTYQCISTTVANKMPVPGNL	235
Qy	242	DQSEPKAKILFW-YVLPISITVFLPSVMGVS-----	272
Db	236	QVDRAGKSYVLKWDYIASADVLFRAQWLPGYSKSSGSHSDKWKPIPTCANVQTHCVFS	295
Qy	273	---IYR---YIHVGKEKHPANLILYGN-----FDKREFVPAEKIVI---NFITLINSDDS	320
Db	296	QDVTYTGTFFLHVQASE-----GNHTSFWSEKFIIDSQKHILPPPPVITWTAMSDT	346
Qy	321	KISH---QDMSLLGKSDVSLNDPQSGNLRPQBEERVKHLGYASHLMEIFCDSEENT	377
Db	347	LLVYVNCQSDTCDGLNVEI-----IFWNTSNT	374
Qy	378	-----EGTSFTQCESLSRTIPDPKTVIEYDVVRTD-----ICAGPEQSELQLOEVS	426
Db	375	KISMEKQGPFTLKNQLPLTVYQVQARVLFRALNKTNSFSEKCEKTRCGSFSTWIIIT	434
Qy	427	TQGTLLSESQAALAVL-----GPTLQ---YSYTFQLQDLPLAQEHTDS-467	
Db	435	GLGVVFSVMVLYALRSWKVYLCHVCPPLKPPSIDEFFSEPPSKNLVLLTAEHTERC	494
Qy	468	-----BEGPEEPSTTLDVWDQDTGRKLCIPSLSSFDQDSEGCPEGSDGLGE	514

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Df      495 FIINTDTVAEVKHAEED-----LRKYSSTQ-----SQDSGNYNNEEBESVGT 539

Dy      515 EGLSLRLYEPE-----ADPRPPGE-----NSTYL 538
        |   :   |   :   ||| 
Dz      540 ESGQAVLSKAPCGGPCSVPSPGTLEDGTCFLGNKYL 577


RESULT 5
interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S27387; S33770
R:Mouchel-Vielh, B.; Lutfallia, G.; Mogenssen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A>Title: Specific antiviral activities of the human alpha interferons are determined at F
A:Reference number: S27387; MUID:93076908; PMID:1446745
A:Accession: S27387
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MOU>
A:Cross-references: UNIPROT:Q04790; UNIPARC:UIP000012D698; EMBL:X68443; NID:g431; PIDN:CAJ
A:Experimental source: MDBK cells
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A>Title: Cloning and characterization of a bovine alpha interferon receptor.
A:Reference number: S33770; MUID:93305725; PMID:8318540
A:Accession: S33770
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421,'V', 423-560 <JJM>
A:Cross-references: UNIPARC:UIP0000167C2D; EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PII
A:Experimental source: lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

Query Match          6.8%; Score 199.5; DB 2; Length 560;
Best Local Similarity 29.1%; Pred. No. 1.5e-06;
Matches    60; Conservative 40; Mismatches    91; Indels   15; Gaps     9;

Dy      19 LLILAAPWGRAVCVSGLLP--KPANITFLSNMKNVQLWTPEGLOGVK-VVTYVQYFIY 76
Dz      10 LMLVAGRW--VLPAASGANLKPNVEITHIIDNFLKNW---SSSESXKVNTFSADIQIL 65

Dy      77 GKQKLNKSECRNTRTYCDLSA-ETSDHYEQYAKVKAIWGTKCSKWAESGRFYPFLET 135
Dz      66 GTDNWKLSGGCHITSYKCNFFSVELENVFKIELRIAREEGNNTSWTEVPFPFLEA 125

Dy      136 QIGPEVALTTDEKSISVVLTAPAERKNRPBDLVPMVMQQIYTNSLNKYNSV-LNTKSNRTW 194
Dz      126 QIGPDFHLEADEAKAILSIISP----KTGDIMWMADR--SSFRSYVVIWNKSSSLEBR 179

Dy      195 SQCVTNHTLVTLWPENTLYGVHVES 220
Dz      180 TETYVPEDKIYK-LSPEITYCLKVKA 204


RESULT 6
interferon gamma receptor precursor - human
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: A31555
R:Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280, 1988
A>Title: Molecular cloning and expression of the human interferon-gamma receptor.
A:Reference number: A31555; MUID:89003065; PMID:2971451
A:Accession: A31555
A:Molecule type: mRNA
A:Residues: 1-489 <AGU>
A:Cross-references: UNIPROT:P15260; UNIPARC:UIP000002CE40; GB:J03143; NID:g184650; PIDN:f
A:Genetics:
```

A;Gene: GDB:IFNGR1; IFNGR  
A;Cross-references: GDB:120688; OMIM:107470  
A;Map position: 6q23-6q24  
C;Superfamily: interferon gamma receptor  
C;Keywords: cytokine receptor; transmembrane protein

Query Match 6.7%; Score 198.5; DB 2; Length 489;  
Best Local Similarity 21.7%; Pred. No. 1.5e-06;  
Matches 104; Conservative 76; Mismatches 199; Indels 101; Gaps 22;

QY 37 LKPNANITELSNMKNVLQW-----TPPEGLQGVKVTYVQYFYIGQK--KWLANKSEC 87  
DB 29 VPTPTNTVIESYNNNDIVYWEYQIMQVP-----VFTVEVKNYGVKNSEWID--AC 77  
QY 88 RNINRYCDLSAETSDYEHQYAKVAIWGTCWKWAEGRFPFLETQIGPEVALTTD 147  
DB 78 INISHHYCNISDHVGDPNSLWVRKARVGQKESAYAKSEFAVCRDGIKPPKGLDIRKE 137  
QY 148 EKSIISVLTAPKWKRNPD-----LPVSMQOIY-----SNLKNVSVLNTKSNRT 193  
DB 138 EKQIMIDIFHPSVFVNGDQEVDDYDPTTCYIRVNVYVMNGSEIQYKI-LTKEDDCD 196  
QY 194 WQCVNTHLVLTWLEPNTLYCVHVESFVPGPRRAQPKQKQCARLTKDOSSEFFAKIIF 253  
DB 197 EIQC-----QLAIPVSSLNSQYCVSAGVLHVWGVTTEKSKVCITIF--NSIKGSL-- 247  
QY 254 WYVLPISITVFLFSVMG--YSIYRYIHVGKEKHPANLILYGNFEFKRFFVPAEKI-VINF 311  
DB 248 W--IPVVAALLFLVLUSLVIFCYI---KKINPLK-----EKSIILPKSLISVRS 293  
QY 312 ITLINISDDSK-----ISHQDMSLLGK-----SSDVSSLNDPQSGNLRPPQE----- 353  
DB 294 AILETKPEKSYVSLITSYQFSLKEVCEPLSPATVPGMTHEDNPGKVEHTEELSSIT 353  
QY 354 -----EEVKHLGYASHLMEIFCDSENTGTSFTQOE--SLSRITPPDKTVIEYDYVR 406  
DB 354 EVVTTENIPDVVPGSHLTPI---ERESSPLSSNQSEPGSIALNSYHSRNCSESDHSRN 410  
QY 407 TTDICAGPEQEQLSQE-----EVSTQGLLESQAALAVLGPQTLOYSVTPOQLD 457  
DB 411 GFDTSSCLESSSHSSUSDSFPPNNKGEIKTEG----QELITVIKAPTSGYDKPHVLVDL 466

RESULT 7  
I56215  
interleukin-10 receptor - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I56215  
R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.  
J. Immunol. 152, 1821-1829, 1994  
A;Title: Expression cloning and characterization of a human IL-10 receptor.  
A;Reference number: I56215; MUID:94165477; PMID:8120391  
A;Status: preliminary;  
A;Molecule type: mRNA  
A;Residues: 1-578 <RES>  
A;Cross-references: UNIPROT:Q13651; UNIPARC:UPI00000012BB; EMBL:U00672; NID:G482802; PID  
C;Genetics:  
A;Gene: GDB:IL10R; HIL-10R  
A;Cross-references: GDB:330958; OMIM:146933  
A;Map position: 11q23.3-11q23.3  
C;Superfamily: interleukin-10 receptor IL10R  
C;Keywords: cytokine receptor

Query Match 6.7%; Score 198.5; DB 2; Length 578;  
Best Local Similarity 21.6%; Pred. No. 1.9e-06;  
Matches 130; Conservative 85; Mismatches 238; Indels 149; Gaps 29;

QY 16 PLLLLLLLAAPWGRVPCVSG--LPKPNANITELSNMKNVLQWTPPEGLQGVKVTYVQY 73  
DB 3 PCLVLLAALLSLRLGSDAHGTLPSPSPWFEAEFFHHILHTWTPIPN-QSSESTCYEVAL 61

A;Gene: GDB:IFNAR1; IFNAR; IFRC  
A;Cross-references: GDB:120078; OMIM:107450  
A;Map position: 21q22.1-21q22.1  
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3  
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein  
F;1-2/Domain: transmembrane #status predicted <TRN1>  
F;437-455/Domain: transmembrane #status predicted <TRN2>  
F;50, 58, 81, 88, 110, 172, 254, 313, 314, 376, 416, 433, 507, 518, 537/Binding site: carbohydrate (As

QY 74 FYIGQKWLKNGEGRNINRYCDLSAETSDYEHQ--YYAKVKAIWGTCWKWAEGRFPY 131  
DB 62 LRYGIESWNSISNCQ-TLSY-DLTAVTLLDLYHSGYRARVRAVDGSRHSNWTVT----- 114  
QY 132 FLETQIGPPEVALTTDEKSI-----SVVLTAPKWKRNPDLPVSMQOIYSNLK-Y 191  
DB 115 --NTRFSPVDEVTLTVGSVNLEIHNGFILGKIQLPRPKMAPAND-----TVESIFSHFREY 167  
QY 182 NVSVLNTKSNRTWSQCVNHT--LVLTWLEPNTLYCVHVESFVPGPRRAQPKQSEKOCART 239  
DB 168 EIAIRKVPQGNFTTTHKKVKHENFSLTSGEVGE-FCVQVKPSVASRSNKGMSKECISL 226  
QY 240 LKQOSEFEKAKIIFWVLPISITVFLFSVMGYSIYRYIHVGKE-----KHPANLIL 290  
DB 227 TRQYFTVTVNVIFFAFVLLLS-----GALACLALQLYVRRKKLPVLLFKKPSFFIF 280  
QY 291 IYG-----NEFDKRFVPAEKIVINFTLINISDDSKISHQDMSLLGKSSDVSSLN 340  
DB 281 ISQRPSPETQDTIHPDLEAEFLKVSPELKN-LDLHGSTDGFGSTKPSLQTEEPQF-LLP 338  
QY 341 DPQPS-----GNLRPQEBEEVKHLGYASHLMEIFCD--SEENTGTSFTQOESLRTIP 393  
DB 339 DHPQADRTLNGEPP-----VLGDCSSGSSNSTSDSGICLQPSLSPSTG 394  
QY 394 PDKTVIEYDYVRTTDICAGPEQEQLSQEYVSTQGLLESQAALAVLGPQTLOYSYTPQ 453  
DB 385 P-----TWEQVQVGSNS--RGQDDSGIDLQV--NSEGRAGDTQ-----GGSALGHHSPP 429  
QY 454 LQ---DLDPDLA---QEHTDSBEGPBEPTTLVDWDPPQTRLCIPLSLSDQDSECEPS 507  
DB 430 PEVPGPEEDPAVAFOGYLQTRCABEKATKT-----GCLBE 465  
QY 508 EG---DGLGEEGLSRLYEAPDRPPGGENETVLMQF-----MEEW 545  
DB 466 ERLPDGLGPK--FGCLVDEAGLHPALAKGYLKQDPLEMTLASSGAPTQGNQPTTEW 523  
QY 546 GL 547  
DB 524 SL 525

RESULT 8  
A32694  
interferon alpha/beta receptor precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: A32694; S17112  
R;Uze, G.; Lutfalla, G.; Gresser, I.  
Cell 60, 225-234, 1990  
A;Title: Genetic transfer of a functional human interferon alpha receptor into mouse cell  
A;Reference number: A32694; MUID:90124632; PMID:2153461  
A;Accession: A32694  
A;Molecule type: mRNA  
A;Residues: 1-557 <UZE>  
A;Cross-references: UNIPROT:PI7181; UNIPARC:UPI000002D51B; GB:J03171; NID:G184645; PIDN:7  
R;Lutfalla, G.  
submitted to the EMBL Data Library, July 1991  
A;Description: The structure of the human interferon alpha/beta receptor gene.  
A;Reference number: S17112  
A;Accession: S17112  
A;Molecule type: DNA  
A;Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>  
A;Cross-references: UNIPARC:UPI0000179801; EMBL:X60459; NID:G32671  
C;Genetics:  
A;Gene: GDB:IFNAR1; IFNAR; IFRC  
A;Cross-references: GDB:120078; OMIM:107450  
A;Map position: 21q22.1-21q22.1  
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3  
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein  
F;1-2/Domain: transmembrane #status predicted <TRN1>  
F;437-455/Domain: transmembrane #status predicted <TRN2>  
F;50, 58, 81, 88, 110, 172, 254, 313, 314, 376, 416, 433, 507, 518, 537/Binding site: carbohydrate (Asr



A49947  
interferon gamma receptor beta subunit - mouse  
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type I  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A49947  
R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.  
Cell 76, 803-810, 1994  
A;Title: A novel member of the interferon receptor family complements functionality of B  
A;Reference number: A49947; MUID:94170381; PMID:8124717  
A;Accession: A49947  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-332 <HEM>  
A;Cross-references: UNIPROT:Q63953; UNIPARC:UPI000022068; GB:S69336; NID:G545841; PIDN:  
A;Experimental source: early B-cell line Y16  
A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)  
C;Keywords: cytokine receptor

Query Match 6.0%; Score 176.5; DB 2; Length 332;  
Best Local Similarity 25.5%; Pred. No. 3.2e-05;  
Matches 71; Conservative 43; Mismatches 129; Indels 35; Gaps 11;

QY 9 LRPLP--LRPLLLLLAAGWRAVPCVSGGLPKPANITFLSINMKNVLQWTP-PEGLOGV 65  
Db 1 MRPLPLPSLLLCGLGA--AASSPDSFSQLAAPLNPRHLHYNDQILTWEPSPSSNDPR 58  
QY 66 KVTYTVQY-FIVGQKKWLKSECRNINRYCDLS--AETSDYEHQY--YAKYKAIWGTK 120  
Db 59 FVYQVEYFIDGSMHRLLEPNCTDITETKCDITGGRLKLFPHPTVFLVRAKRGNT 118  
QY 121 SKWAGSRFPFLETOIGPEVALTTDEKSI SVLTAPEKWKRNPEDLPVSMQIYSLNK 180  
Db 119 SKWVGLPEQHYENVTVGPPKNSIVTPGKSLVIHSP-----VPHGAT 165  
QY 181 YNVSVLNTKSNRTWSQCV----TNHTLVLTWLEPNTLYCVHVESFVPGPPRAQP----S 232  
Db 166 FQYLVHYWEKSETQOQVEGPFKSNIGLVNLPKRYVYCLQTEAQLLNKKIRPHGLLS 225  
QY 233 EKQCARTLKDOSSEFKAKIIFWVLPISITVFLFSVMG 270  
Db 226 NVSCHETTANASARLOOVIL----IFLGIFALLGLTG 259

RESULT 11  
KFRB3  
tissue factor precursor - rabbit  
N;Alternate names: coagulation factor III  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: JU0441; S23681  
R;Andrews, B.S.; Rehemtulla, A.; Fowler, B.J.; Edgington, T.S.; Mackman, N.  
Gene 98, 265-269, 1991  
A;Title: Conservation of tissue factor primary sequence among three mammalian species.  
A;Reference number: JU0441; MUID:91200676; PMID:1840552  
A;Accession: JU0441  
A;Molecule type: mRNA  
A;Residues: 1-292 <AND>  
A;Cross-references: UNIPROT:P24055; UNIPARC:UPI0000136CA5; GB:M55390; NID:G165696; PIDN:  
A;Experimental source: brain  
R;Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.  
Thromb. Haemost. 66, 315-320, 1991  
A;Title: Molecular cloning, characterization and expression of cDNA for rabbit brain tis  
A;Reference number: S23681; MUID:92081032; PMID:1746002  
A;Accession: S23681  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 33-292 <PAW>  
A;Cross-references: UNIPARC:UPI000016C544; EMBL:X53521; NID:G1495; PIDN:CAA37597.1; PID:  
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor  
C;Superfamily: tissue factor  
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolprotein; thiolester bond; transmembrane

F;1-32/Domain: signal sequence #status predicted <SIG>  
F;33-292/Product: tissue factor #status predicted <MAT>  
F;33-249/Domain: extracellular #status predicted <EXT>  
F;250-271/Domain: transmembrane #status predicted <TM>  
F;272-292/Domain: intracellular #status predicted <INT>  
F;41,114,154,167,182/Binding site: carboxydrate (Asn) (covalent) #status predicted  
F;79-87,216-239/Disulfide bonds: #status predicted  
F;274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 5.7%; Score 167; DB 1; Length 292;  
Best Local Similarity 22.5%; Pred. No. 0.00013;  
Matches 70; Conservative 53; Mismatches 126; Indels 62; Gaps 13;

QY 10 RPLPLPPLLLLL--LAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLOGVKV 67  
Db 11 RGTAVPYTVLLGWLAAQVARADTTG----RAYNLTKWSTNFKTILEWEP-----KSIDH 62  
QY 68 TTYTVQYFIVGQKKWLKSECRNINRYCDLSAB-TSDYBHQYVYAKYKAIWGTKS----- 121  
Db 63 VYTVQ--ISTRLENW--KSKCFLTAETECDLTDEVKDVGQTYMARVLSYPARGNTTGGFP 119  
QY 122 ---KWAESGRFPFLETOIGPEVALTTDEKSI SVLTAPEKWKRNPEDLPVSMQIYSN 178  
Db 120 EBPFRNSPEFTPYLDNLGQPTI-----QSFEQVGTKLNVTVQDARTL 163  
QY 179 LKYNVSVLNTKS-----NRT---W-----SQCVTNHTLVLTWLEPNTLYCVHVESFV 222  
Db 164 VRNGTFLSRAVFGKDLNLYYWRASSTGKKTATNTNEFLIDVDKGENYCFVQAVI 223  
QY 223 PGPPRAQSEKQOCARTLKDOSSEFKAKIIFWVLPISITVFLFSVMGYSIVRYIHV--- 279  
Db 224 PSKRKRQRPESLITECTSREQ---RAREMFFIAGVAVVALLIIVLSVTYVKCRKARAG 280  
QY 280 --GKEKHPANL 288  
Db 281 PSKGSSPLNI 291

RESULT 12  
I38500  
interferon gamma receptor accessory factor-1 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: I38500; I38501  
R;Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.I.  
Cell 76, 793-802, 1994  
A;Title: Identification and sequence of an accessory factor required for activation of t  
A;Reference number: A49946; MUID:94170380; PMID:8124716  
A;Accession: I38500  
A;Molecule type: mRNA  
A;Residues: 1-337 <RES>  
A;Cross-references: UNIPROT:P38484; UNIPARC:UPI000012D65E; EMBL:U05875; NID:G463549; PIDN:  
A;Experimental source: clone pSKI  
A;Accession: I38501  
A;Molecule type: mRNA  
A;Residues: 1-63, 'O', 65-337 <RE2>  
A;Cross-references: UNIPARC:UPI00001514B0; EMBL:U05877; NID:G463551; PIDN:AA16956.1; PII  
A;Experimental source: clone pJS3  
C;Genetics:  
C;Keywords: cytokine receptor

Query Match 5.7%; Score 167; DB 2; Length 337;  
Best Local Similarity 23.9%; Pred. No. 0.00016;  
Matches 91; Conservative 49; Mismatches 161; Indels 80; Gaps 18;

QY 9 LRPLPLPPLLLLL--LAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLOGVK- 66  
Db 1 MRPTLLSLLLLLVGFAAAAAPPDPLSQLPAPHPKIRLYNAEQLSWEPVALSNSTRP 60  
QY 67 VYTVQYFIVGQKKWLKSECRNINRYCDLSAETSD-----ECRNINRYCDLSAETSD-----YEHQYVYAKYKAIW 116  
Db 61 VYVRVQ--FKYTDKWNFTADIMSGVNCITQITATEDCTAASPSAGFPMDFNVLRLRAEL 119

```
QY 117 GTCCKWAESGRYPFLETOIGPBE-VALTTDEKSIISVLTAP-----EK 160
Db 120 GALHSAWVTWPFQHRNNTVGPENIEVTPGSGLIIRFSPFDIADTSTAFPCYYVHY
QY 161 WKRPEDLPVSMQOIIYNLKN-VSVLNTKSNRTWSOCVTHVLTWLEPNTLYCVHVE 219
Db 180 WEKG-----GLOQVKGPRFNSISLDNLKPSRVY--CLOVQAQLL-WNKSNIIFRVGHL- 229
QY 220 SFVPGPPRAQPSQKQARTLKQDSSEFKAKIIFWVLPISITVLF-LFSVMGYSIYRYIH 278
Db 230 -----SNISCYETMADASTELQOVL-----ISVGTFSLLSLAGACE----- 267
QY 279 VGKEKHPANLILLYGNEFDKRFVPAEKIVINETILNISDDSKISHQDMSLLGKSSDVSS 338
Db 268 -----FLVLKRYGLIKYWFHTPPS-----IPLQIBEYLKDPQTQPI-LEALDKDSSP 312
QY 339 LNDPQPSGNL--RPPQBEEREV 357
Db 313 KDDVWDSVSIISPFKEQEDV 333

RESULT 13
KF903
tissue factor precursor - bovine
N;Alternate names: coagulation factor III
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1319
R;Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A;Title: cDNA and amino acid sequences of bovine tissue factor.
A;Reference number: JQ1319; MUID:92109720; PMID:1764065
A;Accession: JQ1319
A;Molecule type: mRNA
A;Residues: 1-292 <TAK>
A;Cross-references: UNIPROT:P10931; UNIPARC:UPI0000136CA3; GB:S74147; NID:G241438; PIDN:
A;Experimental source: adrenal gland
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-292/Product: tissue factor #status experimental <MAT>
F;36-248/Domain: extracellular #status predicted <EXT>
F;249-271/Domain: transmembrane #status predicted <TM>
F;272-292/Domain: intracellular #status predicted <INT>
F;43,153,181/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;81-89,215-238/Disulfide bonds: #status predicted
F;118,124/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 5.3%; Score 156; DB 1; Length 292;
Best Local Similarity 22.0%; Pred. No. 0.00082;
Matches 70; Conservative 50; Mismatches 118; Indels 80; Gaps 14;

QY 22 LAAPWGRVPCVSGGLPKPA-----NITFLSINMKVQLQWTPP 59
Db 1 MATPNGRVPCPOAAVARALLFGLVLIQAGVAGTTDVVVAYNITWKSINFKLTLEWEP- 59
QY 60 EGLQGVKVTYVQYFYIGQKKLWLNKSECRNINITYCDLSAE-TSDYEHQYAKVKAIMG 118
Db 60 ---KPINHVYTVQ-ISPRLGNWKNK--CFYTTNTECDVTDIEIKVNRVETYLARVLSYPAD 113
QY 119 KCSKWAEE-----SGRYPFLETOIGPBEVALTTDEKSIISVLTAPKWKRNPELDVSMQ 173
Db 114 TSSSTVEPPFTNSPFTPYLETNLGQFTI-----QSFEQGVGKLVNTVQ 157
QY 174 QIYSNLKNVSNVLTNKS-----NRT-----W-----SOCVTNHTLVLTWLEPNTLYCVH 217
Db 158 DARTLVANSAFSLSDVDVGKDLNLYLYWKASSTKKATNTNGFLDIDVKGNYCFH 217
```

```
QY 218 VSEFVPG--PPRAQPSQKQARTLKQDSSEFKAKIIFWVLPISITVLF-SVMGYSIY 274
Db 218 VQAVILSRNRVRRNKPSPKICTSHEKVLSTE-----LFFIIGTVMVLIIFIVLSVSLH 272
QY 275 RYIHW-----GREKHPAN 287
Db 273 KCRKVRASRGSKENTPLN 290

RESULT 14
KFH03
tissue factor precursor [validated] - human
N;Alternate names: coagulation factor III
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A43645; A47574; A28320; A29062; A29672; A29008
R;Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
Biochemistry 28, 1755-1762, 1989
A;Title: Complete sequence of the human tissue factor gene, a highly regulated cellular
A;Reference number: A43645; MUID:89247359; PMID:2719931
A;Accession: A43645
A;Molecule type: DNA
A;Residues: 1-295 <MAC>
A;Cross-references: UNIPROT:P13726; UNIPARC:UPI000002CD0D; GB:J02846; NID:G339505; PIDN:
R;Fisher, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn, R.M.
Thromb. Res. 48, 89-99, 1987
A;Title: Cloning and expression of human tissue factor cDNA.
A;Reference number: A47574; MUID:88100453; PMID:3424286
A;Accession: A47574
A;Molecule type: mRNA
A;Residues: 1-295 <PIS>
A;Cross-references: UNIPARC:UPI000002CD0D; GB:M27436; NID:G339507; PIDN:AAA36734.1; PID:
R;Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A.; Kraus, J.; Li
Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987
A;Title: Isolation of cDNA clones coding for human tissue factor: primary structure of t
A;Reference number: A94171; MUID:87260946; PMID:3037536
A;Accession: A28320
A;Molecule type: mRNA
A;Residues: 1-295 <SPI>
A;Cross-references: UNIPARC:UPI000002CD0D; GB:J02931; NID:G339501; PIDN:AAA61150.1; PID:
R;Morrissey, J.H.; Fakhrat, H.; Edgington, T.S.
Cell 50, 129-135, 1987
A;Title: Molecular cloning of the cDNA for tissue factor, the cellular receptor for the
A;Reference number: A29062; MUID:87244317; PMID:3297348
A;Accession: A29062
A;Molecule type: mRNA
A;Residues: 1-295 <MOR>
A;Cross-references: UNIPARC:UPI000002CD0D; GB:J02931; NID:G339501; PIDN:AAA61150.1; PID:
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Scarpatti, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.; Flandermeyer, R.R.; Siegel,
Biochemistry 26, 5234-5238, 1987
A;Title: Human tissue factor: cDNA sequence and chromosome localization of the gene.
A;Reference number: A29672; MUID:88050796; PMID:2823875
A;Accession: A29672
A;Molecule type: mRNA
A;Residues: 1-259, A', 261-295 <SCA>
A;Cross-references: UNIPARC:UPI000004E645; GB:M16553; NID:G339503; PIDN:AAA61151.1; PID:
R;Bach, R.; Konigsberg, W.H.; Nemerson, Y.
Biochemistry 27, 4227-4234, 1988
A;Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyto
A;Reference number: A37422; MUID:89000604; PMID:3166978
C;Contents: annotation; disulfide bonds and fatty acid binding site
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor f
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Genetics:
A;Gene: GDB:F3
A;Cross-references: GDB:119895; OMIM:134390
A;Map position: lp22-1p21
A;Introns: 34/1; 71/2; 138/1; 197/3; 251/1
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-295/Product: tissue factor #status experimental <MAT>
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:30:18 ; Search time 197.134 Seconds  
(without alignments)  
1979.144 Million cell updates/sec

Title: US-09-745-792A-11

Perfect score: 2947

Sequence: 1 MRAPGRPALRLPLPLLLL.....NETYLMQFMENGLYQVMEN 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2947	100.0	553	1 I20RA_HUMAN	Q9uhf4 homo sapien
2	1770.5	60.1	546	1 I20RA_MOUSE	Q6pbh0 mus musculus
3	1041.5	35.3	209	2 Q96SH7_HUMAN	Q96sh7 homo sapien
4	470	15.9	568	2 Q800F7_TETNG	Q800f7 tetraodon n
5	469	15.9	568	2 Q800G1_TETNG	Q800g1 tetraodon n
6	444	15.1	591	2 Q575Z1_ONCMY	Q575z1 oncorhynch
7	334.5	11.4	236	2 Q5R1W7_BRARE	Q5r1w7 brachydanio
8	315.5	10.7	229	1 I22RA_RAT	Q7tni4 rattus norv
9	310	10.5	263	1 I22RA_HUMAN	Q969j5 homo sapien
10	294.5	10.0	341	2 Q9YGC8_CHICK	Q9ygc8 gallus gall
11	275	9.3	230	1 I22RA_MOUSE	Q80xf5 mus musculus
12	267.5	9.1	349	1 I10R2_MOUSE	Q6l190 mus musculus
13	261	8.9	351	2 Q8VHM7_MOUSE	Q8vhm7 mus musculus
14	257	8.7	574	2 Q8N6P7_HUMAN	Q8n6p7 homo sapien
15	255	8.7	574	2 Q9H5Z2_HUMAN	Q9hb22 homo sapien
16	254.5	8.6	327	2 Q6ZVU9_HUMAN	Q6zv99 homo sapien
17	253.5	8.6	325	1 I10R2_HUMAN	Q80334 homo sapien
18	253.5	8.6	499	2 Q5PPL5_XENLA	Q5ppl5 xenopus lae
19	242.5	8.2	338	2 Q800G2_TETNG	Q800g2 tetraodon n
20	242	8.2	362	2 Q764M7_PIG	Q764m7 sus scrofa
21	240.5	8.2	502	2 Q5U488_XENLA	Q5u488 xenopus lae
22	239.5	8.1	336	2 Q800E8_TETNG	Q800e8 tetraodon n
23	237	8.0	317	2 Q58CP3_BOVIN	Q58cp3 bos taurus
24	231.5	7.9	581	2 Q80XZ4_MOUSE	Q80xz4 mus musculus
25	225	7.6	575	1 I10R1_MOUSE	Q6l727 mus musculus
26	223.5	7.6	442	2 Q9PVJ9_CHICK	Q9pvj9 gallus gall
27	222.5	7.6	590	1 INAR1_MOUSE	P33896 mus musculus
28	222.5	7.6	590	2 Q80UJ3_MOUSE	Q80uj3 mus musculus
29	220.5	7.5	569	2 Q9YHW0_CHICK	Q9yhw0 gallus gall
30	217.5	7.4	590	2 Q80UR8_MOUSE	Q80ur8 mus musculus
31	215.5	7.3	449	2 Q5XY05_GALLUS	Q5xy05 gallus gall

#### RESULT 1

ID	I20RA_HUMAN	STANDARD;	PRT;	553 AA.
AC	Q9UHf4; Q6UWA9; Q96SH8;			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Interleukin-20 receptor alpha chain precursor (IL-20R-alpha) (IL-20R1)			
DE	(Cytokine receptor family 2 member 8) (Cytokine receptor ciase-II, member 8) (CRF2-8) (ZCYTOR7)			
GN	Names=IL20RA; Synonyms=ZCYTOR7; ORFNames=UNQ681/PRO1315;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).			
RA	Lok S., Kho C., Jelmberg A., Adams R., Whitmore T., Farrah T.,			
RA	O'Hara P.;			
RT	"Homo sapiens cytokine receptor homolog."			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).			
RX	MEDLINE-22987296; PubMed-12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Baton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandien R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,			
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,			
RA	Wood W.I., Godowski P.J., Gray A.M.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003)			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RX	MEDLINE-22935763; PubMed-14574404; DOI=10.1038/nature02055;			
RA	Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,			
RA	Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,			
RA	Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Alnough R.,			
RA	Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,			
RA	Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,			
RA	Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,			
RA	Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,			
RA	Burford D.C., Burrell W., Burton J., Carder C., Carter N.P.,			
RA	Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,			
RA	Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,			
RA	Culley K.M., Dhali P., Davies J., Dunn M., Earthrowl M.E.,			
RA	Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,			
RA	Frankland J., French L., Garner P., Garnett J., Ghori M.J.,			

32	215.5	7.3	569	2	Q5XP11_CHICK	O5xp11 gallus gall
33	211	7.2	333	2	Q7ZT30_TETNG	Q7zt30 tetraodon n
34	209	7.1	560	1	INAR1_PIG	Q764n8 sus scrofa
35	208.5	7.1	305	2	Q6DCU5_XENLA	Q6dcu5 xenopus lae
36	206.5	7.0	203	2	Q7ZT05_TETNG	Q7zt05 tetraodon n
37	205.5	7.0	579	2	Q4KM22_BRARE	Q4km22 brachydanio
38	202	6.9	557	1	INAR1_HUMAN	P17181 homo sapien
39	202	6.9	557	2	Q53H11_HUMAN	Q53h11 homo sapien
40	201	6.8	576	2	Q59F35_HUMAN	Q59f35 homo sapien
41	200.5	6.8	520	1	I28RA_HUMAN	Q8iu57 h interieuk
42	200.5	6.8	520	2	Q5VTX7_HUMAN	Q5vtx7 homo sapien
43	200.5	6.8	569	2	Q99ND6_RAT	Q99nd6 rattus norv
44	199.5	6.8	560	1	INAR1_BOVIN	Q04790 bos taurus
45	199	6.8	508	2	Q9PVK0_CHICK	Q9pvk0 gallus gall

#### ALIGNMENTS

RA Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,  
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,  
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,  
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,  
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,  
RA Kay M., Keenan S.J., Kimberlin A.M., King A., Laird G.K., Langford C.,  
RA Lawlor S., Leongamornlert D.A., Levertha M., Lloyd C.R., Lloyd D.M.,  
RA Loveland J.B., Lovell J., Martin S., Mashreghi-Mohammadi M.,  
RA MacLennan G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,  
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,  
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,  
RA Pearce A.V., Peck A.I., Phillimore B.J.C.F., Phillips S., Plumb R.W.,  
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,  
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,  
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,  
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,  
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L., Wray P.W.,  
RA Whitcaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,  
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,  
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;  
RT "The DNA sequence and analysis of human chromosome 6";  
RL Nature 425:805-811(2003).  
RN [4]  
RP PROTEIN SEQUENCE OF 30-44.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites";  
RL Protein Sci. 13:2819-2824(2004).  
RN [5]  
RP SUBUNIT, LIGAND-BINDING, AND TISSUE SPECIFICITY.  
RX MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;  
RA Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,  
RA Carullo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,  
RA Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,  
RA Prunkard D., Sexson S., Sprecher K., Waggle K., West J.,  
RA Whymore T.E., Yao L., Kuechle M.K., Dalle B.A., Chandrasekher Y.A.;  
RT "Interleukin 20: discovery, receptor identification, and role in  
RT epidermal function";  
RL Cell 104:9-19(2001).  
RN [6]  
RP LIGAND-BINDING.  
RX PubMed=11564763;  
RA Dumoutier L., Leemans C., Lejeune D., Kotenko S.V., Renaud J.-C.;  
RT "STAT activation by IL-19, IL-20 and mda-7 through IL-20 receptor  
RT complexes of two types";  
RL J. Immunol. 167:3545-3549(2001).  
RN [7]  
RP SUBUNIT, AND LIGAND-BINDING.  
RX PubMed=12351624; DOI=10.1074/jbc.M205114200;  
RA Parrish-Novak J., Xu W., Brender T., Yao L., Jones C., West J.,  
RA Brandt C., Jelinek L., Madden K., McKernan P.A., Foster D.C.,  
RA Jaspers S., Chandrasekher Y.A.;  
RT "Interleukins 19, 20, and 24 signal through two distinct receptor  
RT complexes. Differences in receptor-ligand interactions mediate unique  
RT biological functions";  
RL J. Biol. Chem. 277:47517-47523(2002).  
RN [8]  
RP SUBUNIT, AND LIGAND-BINDING.  
RX PubMed=14580208; DOI=10.1021/bi0354583;  
RA Pletnev S., Magracheva E., Kozlov S., Tobin G., Kotenko S.V.,  
RA Wlodawer A., Zdanov A.;  
RT "Characterization of the recombinant extracellular domains of human  
RT interleukin-20 receptors and their complexes with interleukin-19 and  
RT Biochemistry 42:12617-12624(2003).  
RN [9]  
RP SUBUNIT, LIGAND-BINDING, AND TISSUE SPECIFICITY.  
RX PubMed=14764663;  
RA Sheikh F., Baurin V.V., Lewis-Antes A., Shah N.K., Smirnov S.V.,  
RA Anantha S., Dickensheets H., Dumoutier L., Renaud J.-C., Zdanov A.,  
RA Donnelly R.P., Kotenko S.V.;  
RT "IL-26 signals through a novel receptor complex composed of IL-20

receptor 1 and IL-10 receptor 2.";  
RL J. Immunol. 172:2006-2010(2004).  
CC -!- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20 and  
CC IL24. The IL20RA/IL20RB dimer is a receptor for IL26.  
CC -!- SUBUNIT: Heterodimer with IL20RB and heterodimer with IL10RB.  
CC -!- SUBCELLULAR LOCATION: type I membrane protein (by similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9UHF4-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9UHF4-2; Sequence=VSP\_011497, VSP\_011498;  
CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in skin  
CC and testis and high levels in brain. Highly expressed in psoriatic  
CC skin.  
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.  
CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; AF184971; AAF01320.1; -; mRNA.  
CC EMBL; AY358883; AAQ89242.1; -; mRNA.  
CC EMBL; AL135902; CAC38375.1; -; Genomic\_DNA.  
CC HSSP; P13726; 2HFT.  
CC Ensembl; ENSG00000016402; Homo sapiens.  
CC HGNC; HGNC:6003; IL20RA.  
CC MIM; 605620; -;  
CC InterPro; IPR000282; Cytok receptor\_2.  
CC InterPro; IPR003961; FN III.  
CC InterPro; IPR001187; Tissue factor.  
CC Pfam; PF01108; Tissue\_fac; 1.  
CC PROSITE; PS00853; FN3; FALSE NEG.  
CC Alternative splicing; Direct protein sequencing; Glycoprotein;  
KW Receptor; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 29  
FT CHAIN 30 553 Interleukin-20 receptor alpha chain.  
FT TOPO\_DOM 30 250 Extracellular (Potential).  
FT TRANSMEM 251 271 Potential.  
FT TOPO\_DOM 272 553 Cytoplasmic (Potential).  
FT DOMAIN 37 136 Fibronectin type-III 1.  
FT DOMAIN 138 237 Fibronectin type-III 2.  
FT COMEPIAS 353 356 Poly-Glu.  
FT CARBOHYD 42 42 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 83 83 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 91 91 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 182 182 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 191 191 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 200 200 N-linked (GlcNAc... ) (Potential).  
FT DISULFID 87 95 By similarity.  
FT DISULFID 215 236 By similarity.  
FT VARSPPLIC 1 111 Missing (in isoform 2).  
FT VARSPPLIC 112 135 VKAIWGTCKSKWAESGRFPFLET -> MSYNGLHQRFKE  
FT LKILTLCSISS (in isoform 2).  
FT /FTID=VSP\_011498.  
FT CONFLICT 259 259 I -> V (in Ref. 2).  
FT CONFLICT 382 382 F -> L (in Ref. 2 and 3).  
SQ SEQUENCE 553 AA; 625534 MW; 7C23C8543B114659 CRC64;  
Query Match 100.0%; Score 2947; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 1.3e-196;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRAPGRPALRPLPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
DB 1 MRAPGRPALRPLPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
QY 61 GLQGVKVTYVQYFYFYGQKKWLNKSCRNINFTYCDLSAETSDYEHQYAKVAIWGTC 120  
|||||

Db 61 GLOGVKVTYVQYFIYQCKWLKLNCRNINRTYCDLSAETSYEHQYAKVKAIGTKC 120

Qy 121 SKWAESGRFPFPLETOIGPPEVALTTDEKISIVLVTAPEKWKKNPBDLPVSMQOIYSNLK 180

Db 121 SKWAESGRFPFPLETOIGPPEVALTTDEKISIVLVTAPEKWKKNPBDLPVSMQOIYSNLK 180

Qy 181 YNVSVLNTKSNRTWSQCVNTHLTVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240

Db 181 YNVSVLNTKSNRTWSQCVNTHLTVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240

Qy 241 KDOSSEFKAKIIFWYVLPISITVFLFSVMGYSYIRYHVGEKHPANLILYNEFDKRF 300

Db 241 KDOSSEFKAKIIFWYVLPISITVFLFSVMGYSYIRYHVGEKHPANLILYNEFDKRF 300

Qy 301 FVPAEKIVNFIPLNITSDSKISQDMSLGKSSDVSSLNDPQPSGNLRPPQSEKQELS 360

Db 301 FVPAEKIVNFIPLNITSDSKISQDMSLGKSSDVSSLNDPQPSGNLRPPQSEKQELS 360

Qy 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYVDVTTDTCAGPEBQELS 420

Db 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYVDVTTDTCAGPEBQELS 420

Qy 421 LQBEVSTQGTLLRSQALAVLGPQTLOYSYTPQLDPLDPLAQBHTDSEBGPPEPSTTLV 480

Db 421 LQBEVSTQGTLLRSQALAVLGPQTLOYSYTPQLDPLDPLAQBHTDSEBGPPEPSTTLV 480

Qy 481 DNDPQTRGLCIPSLSSFDQDSECEPSEGGDLGEGLLSRLYEAPDRPPGNETYLMQ 540

Db 481 DNDPQTRGLCIPSLSSFDQDSECEPSEGGDLGEGLLSRLYEAPDRPPGNETYLMQ 540

Qy 541 FMEEWGLYQVMEN 553

Db 541 FMEEWGLYQVMEN 553

RESULT 2

I20RA\_MOUSE

ID I20RA\_MOUSE STANDARD; PRT: 546 AA.

AC Q6PHB0; Q8BW64;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Interleukin-20 receptor alpha chain precursor (IL-20R-alpha) (IL-20R1).

GN Name=il20ra;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

[1]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RP STRAIN=C57BL/6J; TISSUE=Oviduct;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Malcais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RT Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

[2]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RP STRAIN=129; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisler F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20 and

IL24. The IL20RA/IL20RB dimer is a receptor for IL26 (By

similarity).

CC -!- SUBUNIT: Heterodimer with IL20RB and heterodimer with IL10RB (By

similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.

CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use as long as its content is in no way modified and this statement is not

removed.

CC -----

DR EMBL; AK054215; BAC35695.1; -; mRNA.

DR EMBL; BC056628; AAH56628.1; -; mRNA.

DR HSSP; P13726; 2HFT.

DR InterPro; IPR000282; Cytok receptor\_2.

DR InterPro; IPR003961; FN\_III.

DR InterPro; IPR001187; Tissue\_factor.

DR Pfam; PF01108; Tissue\_fac; 1.

DR PROSITE; PS00853; FN3; FALSE NEG.

KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.

FT SIGNAL 1 32 Potential.

FT CHAIN 33 546 Interleukin-20 receptor alpha chain.

FT TOPO\_DOM 33 253 Extracellular (Potential).

FT TRANSMEM 254 274 Potential.

FT TOPO\_DOM 275 546 Cytoplasmic (Potential).

FT DOMAIN 33 142 Fibronectin type-III 1.

FT DOMAIN 143 251 Fibronectin type-III 2.

FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 203 203 N-linked (GlcNAc...) (Potential).

FT DISULFID 90 98 By similarity.

FT DISULFID 218 239 By similarity.

FT CONFLICT 145 145 V -> I (in Ref. 2).

DR GO; GO:0004896; F:nematoporetin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.



Db 5 LYIISLWTA VVSDVT-SVAPRKGVHFNMSMLNRNVKWHFCKDPN-DTNTYVEYAIYGR 62  
QY 80 -----KWLKNSKERNINRTYCDLSAETSDYEHQYAKVKAIWCTKCKSWAESGR-FY 130  
Db 63 MDGARRVRLKKKCRDIPQWCDLSNETTDLDEGYFARVAKLGNKGSKWTLTKEKSP 122  
QY 131 PLETOIGPPEVALTTDEKSIISVLTAPKWKRNPEDLFVSMQOIYSNLKYNVSVLNTKS 190  
Db 123 PRADTTFGPPLVKLVVKENSVTVMKGPWRKWTGNMTKEYSLLLKFPQMTYNLSVVDN 182  
QY 191 NRTWSOCVNTHTLVLTWLBENTLYCVHVESFVPGPPRAQPSKQCARILTKQOSSEFKAK 250  
Db 183 NKTQHTFVNRSPEYRLAYETQYCFSAKAVLSLLFACHASWQCLTTSKDPFYQQLLL 242  
QY 251 IIFWYVLPISITVFLFVMSGYSTYRIVHGKKGHPANLLIYGNFEDKRFVPAEKIVN 310  
Db 243 MLGAVVPSVICFLMLILVGLVYHFCVGNKQKSPF-FLEISDIPNPPQTFCEQAVTN 301  
QY 311 FITLNISSDDSK-----ISHQ----- 325  
Db 302 VVLVNVAKPMEMMPINPNTILALIQHSEGEPILPYAAQQAQPGREDCOEGSWEDDFEAQP 361  
QY 326 ----DMSLLGKSDVSLNDPQSGNLRPPQEBEEVHGLVYAS-HL----- 366  
Db 362 EPLEYGFICASPKIPEMRESEASHS-----EETPLLHLQVNMHIAQRSAPCSQGPVEKG 416  
QY 367 ---MEIFCDSEENTECTSTQOESLRTIPDPKTVIEYDVRTT---DICAGPEEQELS 420  
Db 417 LRFMPULSLGKMGESTSYKEPDRVGYP-----QHFSVRETEVDFWEDKABEPOS 469  
QY 421 LOBEVSTQGLLESQAALAVLGPQTLQYS-----YTPQLQDLPLAQHEDTSEEGPBEPS 476  
Db 470 YPSEYETQSNR-----RGTPQLRLQVNLRYRQHTLFPQSEEBEDGSG----- 514  
QY 477 TTLVWDMPOTGRLCIPSLS-----SFDQDSECE--PSEGDGLGSEGLLSRLRYEPAPD 528  
Db 515 -NCVDMSPATTGILQIPLLSKPIPEVNVNRELEQVEILPS-----VVVROSEE---- 560  
QY 529 RPPGENETVLMQFMEEWGLYVQME 552  
Db 561 ---CEGESDLTELQNNWSLVINME 581

RESULT 7  
QSR1W7 BRARE PRELIMINARY; PRT; 236 AA.  
AC QSR1W7;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Novel protein (Fragment).  
GN Name=OTTDARP0000004673; ORNNames=CH211-272F15.1-001;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX072559; CA111965.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:metopioietin/interferon-class (D200-domain. . .; IEA.  
DR InterPro; IPR000282; Cytok\_receptor\_2.  
FT NON TER 236  
SQ SEQUENCE 236 AA; 26811 MW; 11A5DFB03860F85E CRC64;

Query Match 11.4%; Score 334.5; DB 2; Length 236;  
Best Local Similarity 36.2%; Pred. No. 3.7e-15;  
Matches 81; Conservative 41; Mismatches 91; Indels 11; Gaps 4;  
QY 28 RAVPCVSG-GLPRPANITFLSINKNVLQWTPPEGLQGVKVTYVQYFIYG-----Q 78

Db 14 RALSASSADGPPEDRVHVFYSESLRNVVKTAGHGSPTDV-YTVEYAIYGADEKIQE 72  
QY 79 KWLKNSKERNINRTYCDLSAETSDYEHQYAKVKAIWCTKCKSWAES-GRFPPELETQI 137  
Db 73 VWRVPDVCISVQTECDVDSQETFDLRDEYFARVRATSKHGQSVMSIESGRFPLSDTVL 132  
QY 138 GPPEVALTTDEKSIISVLTAPKWKRNPEDLFVSMQOIYSNLKYNVSVLNTKSNRTWSQC 197  
Db 133 GAPLVDVTVRQNHIDITLKGPFWRMKMKKESLWKLIIPNMIYKVSFNSRNRDTPR 192  
QY 198 VTNHTLVLTWLBENTLYCVHVESFVPGPPRAQPSKQCARILTK 241  
Db 193 LINGSLSLGELEFSTQFCVVAQAQSESIPLSVIPSKQCVHTPK 236  
RESULT 8  
I22RA RAT STANDARD; PRT; 229 AA.  
AC Q7TNI4;  
DT 10-MAY-2005 (Rel. 47, Created)  
DT 10-MAY-2005 (Rel. 47, Last sequence update)  
DE Interleukin-22 receptor alpha-2 chain precursor (IL-22R-alpha-2)  
DE (Interleukin 22-binding protein) (IL22BP) (Cytokine receptor family type 2, soluble 1) (CRF2-S1).  
GN Name=IL22ra2;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC STRAIN=Sprague-Dawley; TISSUE=Spleen;  
RX PubMed=15201862; DOI=10.1038/sj.Gene.6364104;  
RA Weiss B., Wolk K., Gruenberg B.H., Volk H.D., Sterry W., Asadullah K., Sabat R.;  
RT "Cloning of murine IL-22 receptor alpha 2 and comparison with its human counterpart."  
RL Genes Immun. 5:330-336(2004).  
CC -!- FUNCTION: Receptor for IL-22. Binds to IL-22, prevents interaction with the functional IL-22R complex and blocks the activity of IL-22 (in vitro). May play an important role as an IL-22 antagonist in the regulation of inflammatory responses.  
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.  
CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC -----  
CC EMBL; AJ555485; CAD88475.1; -; mRNA.  
DR HSSP; P13726; 1JPS.  
DR Ensembl; ENSRNOG00000012259; Rattus norvegicus.  
DR InterPro; IPR000282; Cytok\_receptor\_2.  
DR InterPro; IPR003961; FN\_III.  
DR PROSITE; PS00853; FN3; FALSE NEG.  
KW Glycoprotein; Receptor; Repeat; Signal.  
FT SIGNAL 1 19 By similarity.  
FT CHAIN 20 229 Interleukin-22 receptor alpha-2 chain.  
FT DOMAIN 23 127 Fibronectin type-III 1.  
FT DOMAIN 128 229 Fibronectin type-III 2.  
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).  
FT DISULFID 204 225 By similarity.  
SQ SEQUENCE 229 AA; 26722 MW; 5CFD37652A99365 CRC64;

Query Match 10.7%; Score 315.5; DB 1; Length 229;  
Best Local Similarity 33.8%; Pred. No. 7.4e-14;  
Matches 76; Conservative 32; Mismatches 108; Indels 9; Gaps 4;

QY 17 LLLLLAAPNGRAVPCVSGGLPKPANITFLSINKNKVLQWTPPEGLOGVKVTVYVOYFIY 76  
 DB 9 LLIMLLTATETOPAHVS---LKPQKVOFOSRPNHNLHWPONGNSITNSGVSVPVOYKTY 65  
 QY 77 GQKWLKNSCRNINRTYCDLSAETSDEHYQYAKVKAIAWGTCKSKWAESGRFVPFLEQ 136  
 DB 66 GQGWKDKNDGWTGTFALFCDLTKEITLDPYEPYGRVMAMAGSYSEWTRTPRTPPWETK 125  
 QY 137 IGPEVALTTDEKISISVVLTAPEKKNKPNEDLPVSMQOIYSNLKYNVSLNT---KSNRT 193  
 DB 126 LDPPVVTITRVNASLRVLRPPELPHRNQTKNTMENYI-NLIVRVYSIINNSLEKEQA 184  
 QY 194 WSQCVNHTLVLTWLENTLYCVHVESFVGPFPRAQPSKQCAR 238  
 DB 185 YEG--TORAVEIOGLTHPCSYCVVAEMYQPMFORRSPRSKERCVO 227

RESULT 9

ID 122RA HUMAN STANDARD; Q96A41; Q96QR0; PRT; 263 AA.  
 AC Q96QR0; Q96A41; Q96QR0;  
 DT 10-MAY-2005 (Rel. 47, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Interleukin-22 receptor alpha-2 chain precursor (IL-22R-alpha-2)  
 DE (Interleukin 22-binding protein) (IL22BP) (Cytokine receptor family  
 DE class II member 1) (CRF2-10) (Cytokine receptor family type 2,  
 DE soluble 1) (CRF2-S1).  
 GN Name=IL22RA2; ORFNames=UNQ5793/PRO19598/PRO19822;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.  
 RC TISSUE=Mammary gland, and placenta;  
 RX MEDLINE=21518574; PubMed=11607789; DOI=10.1038/sj.gene.6363786;  
 RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,  
 RA Wolk K., Asadullah K., Sabat R.;  
 RT "A novel, soluble homologue of the human IL-10 receptor with  
 RT preferential expression in placenta.";  
 RL Genes Immun. 2:329-334(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1; 2 AND 3), AND FUNCTION.  
 RX MEDLINE=21286453; PubMed=11390454;  
 RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,  
 RA Dickensheets H., Donnelly R.P., Pestka S.;  
 RT "Identification, cloning, and characterization of a novel soluble  
 RT receptor that binds IL-22 and neutralizes its activity.";  
 RL J. Immunol. 166:7096-7103(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), AND FUNCTION.  
 RC TISSUE=Mammary gland;  
 RX PubMed=11390453;  
 RA Dumoutier L., Lejeune D., Colau D., Renaud J.-C.;  
 RT "Cloning and characterization of IL-22 binding protein, a natural  
 RT antagonist of IL-10-related T cell-derived inducible factor/IL-22.";  
 RL J. Immunol. 166:7090-7095(2001).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.  
 RX MEDLINE=21396522; PubMed=11481447; DOI=10.1073/pnas.171303198;  
 RA Xu W., Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,  
 RA Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer S.,  
 RA Yao L., Whitmore T.E., Chandrasekhar Y., Grant F.J., Maurer M.,  
 RA Jelinek L., Storey H., Brendler T., Hammond A., Topouzis S.,  
 RA Clegg C.H., Foster D.C.;  
 RT "A soluble class II cytokine receptor, IL-22RA2, is a naturally  
 RT occurring IL-22 antagonist.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brueh J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,  
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
 RA Wood W.I., Godowski P.J., Gray A.M.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS PRO-16 AND LYS-190.  
 RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,  
 RA Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;  
 RT "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-  
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;  
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,  
 RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,  
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,  
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,  
 RA Babbage A.K., Baggeley C.L., Bailey J., Banerjee R., Barker D.J.,  
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,  
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,  
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,  
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,  
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,  
 RA Culley K.M., Dhali P., Davies J., Dunn M., Barthrow M.E.,  
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,  
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,  
 RA Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,  
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,  
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,  
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,  
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,  
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,  
 RA Lawlor S., Leongamrert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,  
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,  
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,  
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,  
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,  
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,  
 RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,  
 RA Sahra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,  
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,  
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,  
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,  
 RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,  
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,  
 RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;  
 RT "The DNA sequence and analysis of human chromosome 6.";  
 RL Nature 425:805-811(2003).  
 RN [8]  
 RP PROTEIN SEQUENCE OF 22-36.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824(2004).  
 RN [9]  
 RP TISSUE SPECIFICITY.  
 RX PubMed=15201862; DOI=10.1038/sj.gene.6364104;  
 RA Weiss B., Wolk K., Gruenberg B.H., Volk H.D., Sterry W., Asadullah K.,  
 RA Sabat R.;  
 RT "Cloning of murine IL-22 receptor alpha 2 and comparison with its  
 RT human counterpart.";



Genes Immun. 5:330-336(2004).

[10]

RL SUBCELLULAR LOCATION.

RN MEDLINE=22586333; PubMed=12700595; DOI=10.1038/sj.gene.6363947;

RX Wei C.-C., Ho T.-W., Liang W.-G., Chen G.-Y., Chang M.-S.;

RA "Cloning and characterization of mouse IL-22 binding protein.";

RL Genes Immun. 4:204-211(2003).

CC -!- FUNCTION: Isoform 2 is a receptor for IL-22. Binds to IL-22,

CC prevents interaction with the functional IL-22R complex and blocks

CC the activity of IL-22 (in vitro). May play an important role as an

CC IL-22 antagonist in the regulation of inflammatory responses.

CC Isoform 1 may play a role in establishing and maintaining

CC successful pregnancy.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1; Synonyms=long, CRF2-10L, CRF2-s1-long;

CC IsoId=Q969J5-1; Sequence=Displayed;

CC Name=2; Synonyms=short, CRF2-10, CRF2-s1-short;

CC IsoId=Q969J5-2; Sequence=VSP\_013105;

CC Name=3; Synonyms=CRF2-10S;

CC IsoId=Q969J5-3; Sequence=VSP\_013105, VSP\_013106, VSP\_013107;

CC -!- TISSUE SPECIFICITY: Expressed in placenta, spleen, breast, skin

CC and lung. Also detected in intestinal tract, testis, brain, heart

CC and thymus. No expression found in prostate, bladder, kidney,

CC ovary, muscle, bone marrow, liver and uterus. Isoform 1 is

CC expressed only in placenta. Isoform 2 is expressed in placenta and

CC breast and at lower level in spleen, skin, thymus and stomach.

CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.

CC -!- SIMILARITY: Contains 3 fibronectin type-III domains.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

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CC removed.

CC -----

DR EMBL: AJ313161; CAC85634.1; -; mRNA.

DR EMBL: AJ313162; CAC85635.1; -; mRNA.

DR EMBL: AY040566; AAK85714.1; -; mRNA.

DR EMBL: AY040567; AAK85715.1; -; mRNA.

DR EMBL: AY040568; AAK85716.1; -; mRNA.

DR EMBL: AJ297262; CAC83097.1; -; mRNA.

DR EMBL: AY044429; AAK91775.1; -; mRNA.

DR EMBL: AY358111; AAK88478.1; -; mRNA.

DR EMBL: AY358737; AAQ89097.1; ALT\_INIT; mRNA.

DR EMBL: AY779023; AAV31775.1; -; Genomic\_DNA.

DR EMBL: AL050337; CAI21589.1; -; Genomic\_DNA.

DR EMBL: AL050337; CAI21591.1; -; Genomic\_DNA.

DR EMBL: AL050337; CAI21590.1; -; Genomic\_DNA.

DR HSSP: P24055; 1A21.

DR Ensembl: ENSG0000164485; Homo sapiens.

DR HGNC: HGNC:14901; IL22RA.

DR MIM: 606648; -.

DR InterPro: IPR000282; Cytok receptor\_2.

DR InterPro: IPR003961; FN III.

DR PROSITE: PS50853; FN3; FALSE NEG.

KW Alternative splicing; Direct protein sequencing; Glycoprotein;

KW Polymorphism; Receptor; Repeat; Signal.

FT SIGNAL 1 21

FT CHAIN 22 263 Interleukin-22 receptor alpha-2 chain.

FT DOMAIN 26 68 Fibronectin type-III 1.

FT DOMAIN 100 161 Fibronectin type-III 2.

FT DOMAIN 162 263 Fibronectin type-III 3.

FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).

FT DISULFID 238 259 By similarity.

FT VARSPPLIC 67 98 Missing (in isoform 2 and isoform 3).

FT VARSPPLIC 158 162 Missing (in isoform 3).

FT VARSPPLIC 163 263 Missing (in isoform 3).

FT VARSPPLIC 163 263 Missing (in isoform 3).

FT VARIANT 16 16 L -> P.

FT /FTId=VAR\_021493.

Query Match 10.5%; Score 310; DB 1; Length 263;

Best Local Similarity 32.0%; Pred. No. 2.2e-13;

Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 39 KPNATIFLSINMKNVLTQTPPEGLQGVKVTYTVQYFI----- 75

Db 30 KPRVQVQSRNFHNIQWQPGRALTGNSSVFYQYKIMFSCSMKSSHQKPGCWQHISCN 89

QY 76 -----YGQKWLKSECNINRTYCDLSAETSDYEHQYAKYKAIWGTCKSKWAES 126

Db 90 FFCRTLAKYQGRQWKEDCWGTQELSCDLTSETSDIQEPYVGRVRAASAGSYSEWSMT 149

QY 127 GRFYFPLETQIGPPEVALTTDEKSIWVLTAPEKWRNPEDLPVSMQOQYINLKNVSVL 186

Db 150 PRFTPWETKIDPPVNNITQVNGSLVILHAPNLPYRQYQEKKNVSIEDY-ELLYRVFII 208

QY 187 NTKSNRTSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSKQC 236

Db 209 NNSLEKEQKVEGAHRAVEIALTPHSSYCVAAIYQPMLDRRSORSEERC 259

RESULT 10

QYGC8 CHICK

ID QYGC8\_CHICK PRELIMINARY; PRT; 341 AA.

AC QYGC8;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Interleukin-10 receptor 2.

GN Name=IL10R2;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=99177346; PubMed=10077530;

RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;

RT "Comparative genomic analysis of the interferon/interleukin-10

RT receptor gene cluster.";

RL Genome Res. 9:242-250(1999).

DR EMBL: AF082667; AAD13678.1; -; Genomic\_DNA.

DR EMBL: AF082666; AAD13671.1; -; mRNA.

DR Ensembl: ENSGALG0000015941; Gallus gallus.

DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0016020; C:membrane; IEA.

DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain...; IEA.

DR GO: GO:0004872; F:receptor activity; IEA.

DR GO: GO:0007596; P:blood coagulation; IEA.

DR InterPro: IPR000282; Cytok\_receptor\_2.

DR InterPro: IPR003961; FN III.

DR InterPro: IPR001187; Tissue factor.

DR Pfam: PF01108; Tissue fac.1

DR PRINTS: PR00346; TISSUEFACTOR.

DR SMART: SM00060; FN3; 2.

DR PROSITE: PS50853; FN3; 2.

KW Receptor.

SQ SEQUENCE 341 AA; 39062 MW; 18027239BF8A9C87 CRC64;

Query Match 10.0%; Score 294.5; DB 2; Length 341;

Best Local Similarity 27.6%; Pred. No. 3.8e-12;

Matches 102; Conservative 66; Mismatches 127; Indels 75; Gaps 19;

QY 21 LLAAPMGRAVPCVSGGLPKPATITFLSINKNVLTQTPPEGLQGVKVTYTVQ-YFYTGOK 79

Db 5 LRGLMGCLLLCVSGIVFPRNARISVNFVRSVLLWDPP-GYRKGNLSYTVQAKSIFPKQ 63

QY 80 KWLKSECNINRTYCDLSAETSDYEHQYAKYKAIWGTCKSKWAESGFYPLETQIGP 139



```
Db 64 NFNNVT--TNLNVTECDVSS-LSVY-GAYVLRVTRTEWDESHSDWAVV-RFKPMADTVIGP 118
Qy 140 PEVALTTDEKISVVLTP-----EKWKNPDELVPVSMQIYISNLKYNVSVLNTKSNRT 193
Db 119 PSYNVKSSEGLTVDFGTGPAADREHDKW-----SLKQYYSWIYRILYWKSGSNKK 169
Qy 194 WSQCVTNH-TLVLTWLEPNTLYCVHVESFVPGPPRAAPSEKOCARTLKDOSSEFRKAKII 252
Db 170 VIHIDTKHNEIISQLSEPTIYCIQVGVIPENWKTGERSQELCEQTHNGVTP----- 223
Qy 253 FWYVLPISITVFLSVSMG-----YSIYRIYHVGKEKH-----PANILILIY 292
Db 224 VWIV-----VTVLGSLMAVIVSPVCFPAFWLYRP-----TKHVFPPSYIFFOHL---- 270
Qy 293 GNEFDKRFVPA---EKVINPFTLISDDSKISHQDMSLLGKSSDVSSLNDPQ----PSG 346
Db 271 -----KEFFSPVQEEHFFHDLTV-ISEEPK-SQRDETVEEASRTAEHHQDSKQBISDS 323
Qy 347 NLRPPQOEIEE 356
Db 324 EILPPLERDQ 333

RESULT 11
I22RA MOUSE
ID I22RA MOUSE STANDARD; PRT; 230 AA.
AC Q80XF5; Q7TNIS;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-22 receptor alpha-2 chain precursor (IL-22R-alpha-2)
DE (Interleukin 22-binding protein) (IL22BP) (Cytokine receptor family
DE type 2, soluble 1) (CRF2-S1).
GN Name=IL22ra2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutharia; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND SUBCELLULAR LOCATION.
RX STRAIN=BALB/c;
RX MEDLINE=22586333; PubMed=12700595; DOI=10.1038/sj.gene.6363947;
RA Wei C.-C., Ho R.-W., Liang W.-G., Chen G.-Y., Chang M.-S.;
RT "Cloning and characterization of mouse IL-22 binding protein.";
RL Genes Immun. 4:204-211(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RC STRAIN=BALB/c; TISSUE=Spleen;
RX PubMed=15201862; DOI=10.1038/sj.gene.6364104;
RA Weiss B., Wolk K., Gruenberg B.H., Volk H.D., Sterry W., Asadullah K.,
RA Sabat R.;
RT "Cloning of murine IL-22 receptor alpha 2 and comparison with its
RT human counterpart.";
RL Genes Immun. 5:330-336(2004).
CC -1- FUNCTION: Receptor for IL-22. Binds to IL-22, prevents interaction
CC with the functional IL-22R complex and blocks the activity of IL-
CC 22 (in vitro). May play an important role as an IL-22 antagonist
CC in the regulation of inflammatory responses.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highly expressed in lymph nodes and at lower
CC levels in lung, spleen, and thymus. Not expressed in kidney, liver
CC and heart.
CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -1- SIMILARITY: Contains 2 fibronectin type-III domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF493604; AAP13730.1; -; mRNA.
```

```
DR EMBL; AJ555484; CAD88474.1; -; mRNA.
DR HSSP; P13726; 1JPS.
DR Ensembl; ENSMUSG00000039760; Mus musculus.
DR MGI; MGI:2665114; IL22ra2.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0045515; P:protein binding; IPI.
DR GO; GO:0042516; P:regulation of tyrosine phosphorylation of S...; IDA.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR003961; FN_III.
DR PROSITE; PS0853; FN3; FALSE_NEG.
DR Receptor; Repeat; Signal.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 230 Interleukin-22 receptor alpha-2 chain.
FT DOMAIN 30 128 Fibronectin type-III 1.
FT DOMAIN 129 230 Fibronectin type-III 2.
FT DISULFID 205 226 By similarity.
FT CONFLICT 149 149 D -> E (in Ref. 2).
FT CONFLICT 228 228 Q -> H (in Ref. 2).
SQ SEQUENCE 230 AA; 26589 MW; 9AEA29768A756A75 CRC64;

Query Match 9.3%; Score 275; DB 1; Length 230;
Best Local Similarity 31.7%; Pred. No. 4.9e-11;
Matches 64; Conservative 32; Mismatches 100; Indels 6; Gaps 3;

Qy 40 PANITFLSINMKVQLQWTPPEGLQGVKVTYVQYFYGQKKWLKSECRNINRYCDLSA 99
Db 30 PQKVRFSQSRNFHILHWQAGSSLPNNSIYFVQYKMGQSQWEDKVCWCTTALFCDLTN 89
Qy 100 ETSYDEHYQYAKAIWGTGKCKWAESGRFPFPELETQIGPPEVALTTDEKISVVLTAPE 159
Db 90 ETLLDPVELYIGRVMTACAGHSAWTRTPRTPWETKLDPPVVTITRVNASLRLVLRPPD 149
Qy 160 KWKRPEDLPVSMQIYISNLKYNVSVLNT---KSNRTWSQCVTNHILVLTWLEPNTLYCV 216
Db 150 LPNRNOSGKNASMETYY-GLVYRVFTINNSLEKEQKAYEG--TORAVEIEGLPHSSYCV 205
Qy 217 HVESFVPGPPRAAPSEKOCAR 238
Db 207 VAEWYQPMFDRSPRSKRCVCVQ 228

RESULT 12
I10R2 MOUSE
ID I10R2 MOUSE STANDARD; PRT; 349 AA.
AC Q61190;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DE (Cytokine receptor family 2 member 4) (Cytokine receptor class-II,
DE member 4) (CRF2-4).
GN Name=il10rb; Synonyms=Crfb4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutharia; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97199375; PubMed=9047351; DOI=10.1016/S0378-1119(96)00690-7;
RA Gibbs V.C., Pennica D.;
RT "CRF2-4: isolation of cDNA clones encoding the human and mouse
RT proteins.";
RL Gene 186:97-101(1997).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=98130620; PubMed=9463407; DOI=10.1084/jem.187.4.571;
RA Spencer S.D., Di Marco F., Hootley J., Pitts-Week S., Bauer M.,
RA Ryan A.M., Sordat B., Gibbs V.C., Aguet M.;
RT "The orphan receptor CRF2-4 is an essential subunit of the interleukin
RT 10 receptor.";
RL J. Exp. Med. 187:571-578(1998).
CC -1- FUNCTION: Receptor for IL10 and IL22. Serves as an accessory chain
```

```
CC essential for the active IL10 receptor complex and to initiate
CC IL10-induced signal transduction events.
CC -l- SUBCELLULAR LOCATION: Type I membrane protein.
CC -l- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -l- SIMILARITY: Contains 2 fibronectin type-III domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U53696; AAC3062.1; -; mRNA.
DR Ensembl; ENSMUSG00000022969; Mus musculus.
DR MGI; MGI:109380; Il10rb.
DR GO; GO:0004920; F:interleukin-10 receptor activity; IMP.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR001187; FN_III.
DR PRINTS; PR00346; TISSUEFACTOR.
DR PROSITE; PS50853; FN3; 2.
DR Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
KW SIGNAL
FT CHAIN 1 19 Potential.
FT TOPO_DOM 20 349 Interleukin-10 receptor beta chain.
FT TRANSMEM 21 220 Extracellular (Potential).
FT TOPO_DOM 22 241 Potential.
FT DOMAIN 22 107 Cytoplasmic (Potential).
FT DOMAIN 111 208 Fibronectin type-III 1.
FT CARBOHYD 49 49 Fibronectin type-III 2.
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 199 199 N-linked (GlcNAc...) (Potential).
FT DISULFID 66 74 By similarity.
FT DISULFID 188 209 By similarity.
SQ SEQUENCE 349 AA; 39774 MW; 58BA4F6B86330A39 CRC64;

Query Match 9.1%; Score 267.5; DB 1; Length 349;
Best Local Similarity 27.3%; Pred. No. 3e-10;
Matches 98; Conservative 53; Mismatches 157; Indels 51; Gaps 15;

QY 31 PCVSGGL-----PKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYQG 78
Db 3 PCVAGWLGGLLVPALGMIPPPPEKVRMNSVFNKILQWEP-APPKTNLTFTAQYESYRS 61
QY 79 KKWLNKSECRNINRTYCDLSAETSDEHYQYAKVKAIWGTCSCWAESGRFYPLETQIG 138
Db 62 ----FQDHCKRTASTQCDFS-HLSKY-GDYTVRVRAELADEHSEWV-NVTFPCPVEDTIIG 114
QY 139 PREVALTTDEKTSVLTAPKWKRNPEDLVSMQOIYSNLYKYNVSVLNTKSNRTWSQCV 198
Db 115 PPEMQTESLAESLHRSAPQ-IENEPETW--TLKNIYDSWAYRVQWKNGTNEKFPQVVS 171
QY 199 TNHTLVLTWLEPNTLYCVHVESFVPGPPRAQSEKOCARTLKQDSSEFKAKIIFWVLP 258
Db 172 PYDSEVLRLNLEPWTTCIQVQGLLDQNRGTGESEPICERTGND---EITPSWIVAILI 228
QY 259 ISITVFLFSVMGYSIYRIYHVGKEKH-----PANLILYGNFDPKRF----FVPAEK 306
Db 229 VSVLVVFLFLGCFVFLIYKTKHTFRSGTSLPQHLKEFLGHPHHSTFLFPFPPEP 288
QY 307 IVINFTITANI---SDDSKISHODMSLLGKSSDVS-----SLNDPQPSGNLRPPQEEV 357
Db 289 AEV-FDKLSIISESGSKQSPEDNCASEPSPDGPPELESKDEAPS-----PPHDDPKL 342

RESULT 13
Q8VHM7_MOUSE
ID Q8VHM7_MOUSE PRELIMINARY; PRT; 351 AA.
AC Q8VHM7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
```

```
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 10 receptor 2 precursor.
GN Names:Il10rb; Synonyms=Il10r2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Hardy M.P.; Hertzog P.J.; Owczarek C.M.;
RT "The genomic structure and expression patterns of the gene encoding
RL the second chain of the murine interleukin 10 receptor, IL-10R2."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440787; AAL40946.1; -; mRNA.
DR PIR; JC6311; JC6311.
DR Ensembl; ENSMUSG00000022969; Mus musculus.
DR MGI; MGI:109380; Il10rb.
DR GO; GO:0004920; F:interleukin-10 receptor activity; IMP.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR001187; Tissue_factor.
DR PRINTS; PR00346; TISSUEFACTOR.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
KW Receptor; Signal; Transmembrane.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 351 AA; 40031 MW; 53102D95809AF5D0 CRC64;

Query Match 8.9%; Score 261; DB 2; Length 351;
Best Local Similarity 27.6%; Pred. No. 8.6e-10;
Matches 96; Conservative 54; Mismatches 158; Indels 40; Gaps 15;

QY 30 PCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYQKKWLNKSECRN 89
Db 17 VPAL-GMIPPPPEKVRMNSVFNKILQWEP-APPKTNLTFTAQYESYRS----FQDHCKR 70
QY 90 INRTYCDLSAETSDEHYQYAKVKAIWGTCSCWAESGRFYPLETQIGPEVALTTDEK 149
Db 71 TASTQCDFS-HLSKY-GDYTVRVRAELADEHSEWV-NVTFPCPVEDTIIGPEMQIESLAE 127
QY 150 SISVLTAPKWKRNPEDLVSMQOIYSNLYKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 209
Db 128 SLHLRSAPQ-IENEPETW--TLKNIYDSWAYRVQWKNGTNEKFKQVSYDSEVLRLNLE 184
QY 210 PNTLYCVHVESFVPGPPRAQSEKOCARTLKQDSSEFKAKIIFWVLPISITVFLFSVM 269
Db 185 PWTTCIQVQGLLDQNRGTGESEPICERTGND---EITPSWIVAILIIVSVLVWFLFL 241
QY 270 GYSIYRIYHVGKEKH-----PANLILYGNFDPKRF----FVPAEKIVINFTITANI- 316
Db 242 GCFVVLWLIYKTKHTFRSGTSLPQHLKEFLGHPHHSTFLFPFPPEAEV-FDKLSII 300
QY 317 ---SDDSKISHODMSLLGKSSDVS-----SLNDPQPSGNLRPPQEEV 357
Db 301 SESESGSKQSPEDNCASEPSPDGPPELESKDEAPS-----PPHDDPKL 344

RESULT 14
Q8N6P7_HUMAN
ID Q8N6P7_HUMAN PRELIMINARY; PRT; 574 AA.
AC Q8N6P7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Interleukin 22 receptor, alpha 1.
GN Name=IL22RA1; ORFName=RP11-293P20.5-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
```

```

OX NCBI_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adrenal cortex;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RA Chapman J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE.
RA Lad H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029273; AAH29273.1; -; mRNA.
DR EMBL; AL590683; CAH70116.1; -; Genomic DNA.
DR EMBL; AL591178; CAH72088.1; -; Genomic DNA.
DR EMBL; AL591178; CAH70116.1; JOINED; Genomic DNA.
DR EMBL; AL590683; CAH72088.1; JOINED; Genomic DNA.
DR HSSP; PI3726; ITFH.
DR Ensembl; ENSG00000142677; Homo sapiens.
DR HGNC; HGNC:13700; IL22RA1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; Cytok_receptor_2.
DR ProSite; PS50853; FN3; I.
DR Receptor; Repeat; Transmembrane.
SQ SEQUENCE 574 AA; 63077 MW; D46CC71D496F3420 CRC64;

Query Match 8.7%; Score 257; DB 2; Length 574;
Best Local Similarity 22.7%; Pred. No. 3.3e-09;
Matches 134; Conservative 93; Mismatches 243; Indels 120; Gaps 28;

QY 42 NITFLSINMKNVLQW--TPPEGLQGVKVTYVQYFIYQCKWLNKSECRNINRYCDLSAE 100
DB 27 HVKFSQSNFENILTWDSGPEGTP--DTVYSIEYKTYGERDWVAKGQCRITRKSCLNLTVE 84

QY 101 TSDYEHQYVAKVKAIGWTKSKWAESGRFFPFLETOIGPPEVALTTDEKSIISVLTAPKE 160
DB 85 TGNLTLYYARVTVAVSAGRSATKMTDRFSSLOHTLTKPDVTCISKVRSIQMIV----- 139

QY 161 WKNPNEDLPV-----SMQYISNLYKNVSVLNTKSNRTWSQCV--TNHTLVLTWLEP 210
DB 140 ---HPTPTPIRAGDGHRLTLEDIFHDLFYH---LELQVNRVYQWHLGGKQREYEFGLTP 193

QY 211 NTLVYCHVRSFVGPFPRAQPSKQC-ARTLKQDSSEFAKAIIFWVLPISIVTFLPSVM 269
DB 211 NTLVYCHVRSFVGPFPRAQPSKQC-ARTLKQDSSEFAKAIIFWVLPISIVTFLPSVM 269

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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:29:48 ; Search time 209.295 Seconds

(without alignments)  
1160.927 Million cell updates/sec

Title: US-09-745-792a-11

Perfect score: 2947

Sequence: 1 MRAPGRPALRLPLPLLLL.....NETYLMQFMEWGLYVQWEN 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2947	100.0	553	2 AAW79159	Aaw79159 Zcytor7 c
2	2947	100.0	553	4 AAB85268	Aab85268 Human IL-
3	2947	100.0	553	4 AAU04058	Aau04058 Human int
4	2947	100.0	553	5 ABG67199	Abg67199 Human int
5	2947	100.0	553	5 AAE23353	Aae23353 Human int
6	2947	100.0	553	6 ABR38943	Abr38943 Human AK1
7	2947	100.0	553	6 ABP70950	Abp70950 Interleuk
8	2947	100.0	553	8 ADJ83291	Adj83291 Human int
9	2947	100.0	553	8 ADJ75638	Adj75638 Marker ge
10	2947	100.0	553	8 ADN04874	Adn04874 Antipsori
11	2947	100.0	553	9 ADW64528	Adw64528 Human IL-
12	2947	100.0	553	9 AEA50101	Aea50101 Mouse IL-
13	2947	100.0	553	9 AEA50061	Aea50061 Human IL-
14	2947	100.0	553	9 AEA50099	Aea50099 Mouse IL-
15	2947	100.0	553	9 AEA50103	Aea50103 Mouse IL-
16	2947	100.0	553	9 AEA28837	Aea28837 Human/mou
17	2947	100.0	553	9 AEA28841	Aea28841 House mou
18	2947	100.0	553	9 AEA28839	Aea28839 House mou
19	2947	100.0	553	9 AEA28799	Aea28799 Human int
20	2947	99.9	553	6 ABR38947	Abr38947 Human AK1
21	2943	99.9	553	6 ABR38946	Abr38946 Human AK1
22	2941	99.8	553	4 ABB11582	Abb11582 Human cla
23	2941	99.8	553	8 ADM95033	Adm95033 Human int
24	2941	99.8	553	9 AEA00133	Aea00133 Human TAT

25	2941	99.8	553	9 AEA00653	Aea00653 Human TAT
26	2937	99.7	553	6 ABR38948	Abr38948 Human AK1
27	2880	97.7	542	4 AAUI2265	Aaul2265 Human PRO
28	2880	97.7	542	4 AAU29222	Aau29222 Human PRO
29	2880	97.7	542	6 ABUS5858	Abu58598 Human PRO
30	2880	97.7	542	6 ABUS88146	Abu88146 Novel hum
31	2880	97.7	542	6 ABUS84461	Abu84461 Human sec
32	2880	97.7	542	6 ABR66335	Abr66335 Human sec
33	2880	97.7	542	6 ABR65725	Abr65725 Human sec
34	2880	97.7	542	6 ABUS9665	Abu99665 Human sec
35	2880	97.7	542	6 ABUS2904	Abu82904 Human PRO
36	2880	97.7	542	6 ABO17709	Abol17709 Novel hum
37	2880	97.7	542	6 ABUS90025	Abu90025 Novel hum
38	2880	97.7	542	6 ABR68274	Abr68274 Human sec
39	2880	97.7	542	6 ABUS6327	Abu96327 Novel hum
40	2880	97.7	542	6 ABUS2758	Abu92758 Human sec
41	2880	97.7	542	6 ABO08835	Abo08835 Human sec
42	2880	97.7	542	6 ABO02887	Abo02887 Human sec
43	2880	97.7	542	6 ABR75041	Abr75041 Human sec
44	2880	97.7	542	6 ABR94803	Abr94803 Human sec
45	2880	97.7	542	6 ABUS5776	Abu85776 Human PRO

#### ALIGNMENTS

##### RESULT 1

AAW79159

ID AAW79159 standard; protein; 553 AA.

XX AC AAW79159;

XX AC AAW79159;

DT 20-NOV-1998 (first entry)

XX Zcytor7 cytokine receptor polypeptide.

XX Zcytor7 cytokine receptor polypeptide.

KW Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;

KW type 2 cytokine receptor family; CRP2; prostate tissue; nervous tissue;

KW agonist; cell proliferation; cell differentiation; renal disease; human;

KW neural disease; pancreatic disease.

XX Homo sapiens.

XX Homo sapiens.

XX Key

XX Domain

XX Location/Qualifiers

XX 30..250

XX /note= "extracellular (ligand-binding) domain; sequence

XX claimed in claim 1"

XX Domain

XX 275..553

XX /note= "intracellular domain"

XX WO9837193-A1.

XX 27-AUG-1998

XX 18-FEB-1998; 98WO-US003029.

XX 20-FEB-1997; 97US-00803305.

XX 02-OCT-1997; 97US-00943087.

XX (ZYMO ) ZYMOGENETICS INC.

XX Lok S; Kho CJ, Jelmsberg AC, Adams RL, Whitmore TE, Farrah TM;

XX WPI; 1998-480798/41.

XX N-PSDB; AAV57515.

XX Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful for

XX treating renal, neural, pancreatic and prostatic diseases.

XX Claim 1; Page 55-59; 72pp; English.

XX This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-

XX binding receptor polypeptide and is a novel member of the type 2 cytokine

CC

CC receptor family (CRF2). An expression vector containing the Zcytor  
CC polynucleotide, operably linked to transcription promoter, a sequence  
CC encoding a transmembrane and intracellular domain, or both, and a  
CC transcriptional terminator can be used to transform host cells for the  
CC recombinant production of the polypeptide. The sequences can be used to  
CC study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is  
CC preferentially expressed in the kidney, pancreas, prostate or nervous  
CC tissue. Agonists of Zcytor7 can be used to stimulate proliferation and  
CC differentiation of cell in these organs. The antagonists and agonists can  
CC also be used in the treatment of renal, neural, pancreatic and prostate  
CC diseases  
XX  
SQ Sequence 553 AA;  
  
Query Match 100.0%; Score 2947; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 5.6e-240;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60  
Db 1 MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60  
  
QY 61 GLOGVKVTYTVQYFIYGQKKWLKNSCRNINRTYCDLSAETSDEYHGYAKVKAIWGTC 120  
Db 61 GLOGVKVTYTVQYFIYGQKKWLKNSCRNINRTYCDLSAETSDEYHGYAKVKAIWGTC 120  
  
QY 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYSNLK 180  
Db 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYSNLK 180  
  
QY 181 YNVSVLTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGP PRRAPQSEKQCARTL 240  
Db 181 YNVSVLTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGP PRRAPQSEKQCARTL 240  
  
QY 241 KDQSSBFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDKRF 300  
Db 241 KDQSSBFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDKRF 300  
  
QY 301 FVPAEKIVINFITLNI SDQSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360  
Db 301 FVPAEKIVINFITLNI SDQSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360  
  
QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVRTTICAGPEQELS 420  
Db 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVRTTICAGPEQELS 420  
  
QY 421 LQBEVSTQGTLLSQAAALAVLGPOTLQYSYTPQLQDLPLAQBSHTDSEEGPEEPSTTLV 480  
Db 421 LQBEVSTQGTLLSQAAALAVLGPOTLQYSYTPQLQDLPLAQBSHTDSEEGPEEPSTTLV 480  
  
QY 481 DWDPQTRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEAPDRPPGNETYLMQ 540  
Db 481 DWDPQTRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEAPDRPPGNETYLMQ 540  
  
QY 541 FMEEWGLYVOMEN 553  
Db 541 FMEEWGLYVOMEN 553  
  
RESULT 2  
AAB85268  
ID AAB85268 standard; protein; 553 AA.  
XX  
AC AAB85268;  
XX  
DT 07-SEP-2001 (first entry)  
XX  
DE Human IL-20 receptor subunit IL-20RA.  
XX  
KW Interleukin 20; IL-20; IL-20RA; Zcytor7; IL-20RB; DIRS1; immunoglobulin;  
KW antiinflammatory; antipsoriatic; antiasthmatic; antibacterial; human;  
KW dermatological; antiulcer; antagonist.  
XX

OS Homo sapiens.  
XX WO200146232-A2.  
XX  
XX 28-JUN-2001.  
XX  
PD 22-DEC-2000; 2000WO-US035307.  
PF 23-DEC-1999; 99US-00471774.  
XX  
PR 22-JUN-2000; 2000US-0213416P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;  
PI Rixon MW, Presnell SR, Fox BA;  
XX  
XX WPI; 2001-398320/42.  
DR N-PSDB; AAH22815.  
XX  
XX Isolated interleukin 20 soluble receptor comprising two polypeptide  
PT subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus  
PT treating inflammatory diseases such as psoriasis.  
XX  
XX Disclosure; Page 63-65; 119pp; English.  
XX  
XX The invention relates to an interleukin 20 (IL-20) soluble receptor  
CC comprising two polypeptide subunits IL-20RA (formerly known as Zcytor7)  
CC and IL-20RB (formerly known as DIRS1). The two subunits are preferably  
CC linked together. In one embodiment, one subunit is fused to the constant  
CC region of the light chain of an immunoglobulin, and the other subunit is  
CC fused to constant region of the heavy chain of an immunoglobulin. The  
CC light chain and the heavy chain are connected via a disulphide bond. The  
CC soluble receptor can be used to down-regulate IL-20 and thus treat  
CC inflammatory diseases such as psoriasis, inflammatory lung injury such as  
CC asthma or bronchitis, adult respiratory disease (ARD), septic shock,  
CC multiple organ failure, bacterial pneumonia, eczema, atopic and contact  
CC dermatitis, and inflammatory bowel disease such as ulcerative colitis and  
CC Crohn's disease. The present sequence represents a human IL-20 receptor  
CC subunit IL-20RA  
XX  
SQ Sequence 553 AA;  
  
Query Match 100.0%; Score 2947; DB 4; Length 553;  
Best Local Similarity 100.0%; Pred. No. 5.6e-240;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60  
Db 1 MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60  
  
QY 61 GLOGVKVTYTVQYFIYGQKKWLKNSCRNINRTYCDLSAETSDEYHGYAKVKAIWGTC 120  
Db 61 GLOGVKVTYTVQYFIYGQKKWLKNSCRNINRTYCDLSAETSDEYHGYAKVKAIWGTC 120  
  
QY 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYSNLK 180  
Db 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYSNLK 180  
  
QY 181 YNVSVLTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGP PRRAPQSEKQCARTL 240  
Db 181 YNVSVLTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGP PRRAPQSEKQCARTL 240  
  
QY 241 KDQSSBFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDKRF 300  
Db 241 KDQSSBFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDKRF 300  
  
QY 301 FVPAEKIVINFITLNI SDQSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360  
Db 301 FVPAEKIVINFITLNI SDQSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360  
  
QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVRTTICAGPEQELS 420  
Db 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVRTTICAGPEQELS 420



XX 23-DEC-1999; 99US-0171969P.  
PR 22-JUN-2000; 2000US-0213341P.  
XX (THOM/) THOMPSON P.  
PA (FOST/) FOSTER D C.  
PA (KUMW/) XU W.  
PA (MADD/) MADDEN K L.  
PA (KELL/) KELLY J D.  
PA (SPRE/) SPRECHER C A.  
PA (BLUM/) BLUMBERG H.  
PA (EAGA/) EAGAN M A.  
PA (JASP/) JASPERS S R.  
PA (CHAN/) CHANDRASEKHAR Y A.  
PA (NOVA/) NOVAK J E.  
XX Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA;  
PI Blumberg H, Eagan MA, Jaspers SR, Chandrasekhar YA, Novak JE;  
XX N-PSDB; ABR96176.  
DR WPI: 2002-507215/54.  
XX N-PSDB; ABR96176.  
XX Treating inflammatory skin and lung diseases using antibodies against  
PT interleukins (IL)-20 (which indirectly modulates activation of IL-8),  
PT useful for treating e.g. psoriasis, asthma and bronchitis.  
XX Disclosure; Page 20-21; 68pp; English.  
XX The invention describes a method (I) for treating a mammal afflicted with  
CC a disease in which an interleukin-20 (IL-20) polypeptide plays a role  
CC comprising administering antagonist of the IL-20 polypeptide to the  
CC individual. An important cytokine in the inflammatory process is  
CC interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils  
CC via chemotaxis and the release of granule enzymes. IL-8 binds to  
CC receptors on neutrophils, monocytes, basophils, and eosinophils. IL-8 is  
CC a potent chemoattractant for neutrophils; and the early stages of  
CC periodontal disease are characterised by the influx of neutrophils. IL-8  
CC is a potent inducer of angiogenesis in several angiogenesis-dependent  
CC chronic inflammatory conditions, including rheumatoid arthritis.  
CC psoriasis, and idiopathic pulmonary fibrosis. Additionally, IL-8 is an  
CC important source of angiogenic activity in human lung cancer. Also, IL-8  
CC expression correlates with experimental metastatic activity of some  
CC melanoma cell lines. Therefore an effective method to treat inflammatory  
CC diseases would be to administer an agent that would inhibit IL-8. It has  
CC been shown that IL-20 up-regulates IL-8. Therefore antagonists to IL-20  
CC can be used to treat these diseases. The method is used for treating  
CC diseases in which the IL-20 polypeptide plays a role e.g. inflammatory  
CC diseases including diabetes, arteriosclerosis, cataracts, reperfusion  
CC injury, cancer, meningitis, rheumatic diseases, idiopathic pulmonary  
CC fibrosis, inflammatory bowel disease (ulcerative colitis), skin disease  
CC (psoriasis, eczema, atopic dermatitis and contact dermatitis) or an  
CC inflammatory lung disease (adult respiratory disease (ARD), asthma,  
CC bronchitis and pneumonia). This sequence represents a human interleukin-  
CC 20 (IL-20) polypeptide used in developing the method of the invention  
XX Sequence 553 AA;  
XX Query Match 100.0%; Score 2947; DB 5; Length 553;  
Best Local Similarity 100.0%; Pred. No. 5.6e-240;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRAPGRPALRPLPPLLLLLLAAPGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
Db 1 MRAPGRPALRPLPPLLLLLLAAPGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
QY 61 GLQGVKVTYTVQYFIYGQKWLNKSCRNINRTYCDLSAETSDEHYQYAKVKAIWGTRC 120  
Db 61 GLQGVKVTYTVQYFIYGQKWLNKSCRNINRTYCDLSAETSDEHYQYAKVKAIWGTRC 120  
QY 121 SKWAESGRYPFLETOIGPPEVALTTDEKSIISVLTAPKWKNPEDLPVSMQOIIYSNLK 180  
Db 121 SKWAESGRYPFLETOIGPPEVALTTDEKSIISVLTAPKWKNPEDLPVSMQOIIYSNLK 180

QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPSPRRAPQSEKQCARTL 240  
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPSPRRAPQSEKQCARTL 240  
QY 241 KQOSSEFKAKIIFWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILYGNEDKRF 300  
Db 241 KQOSSEFKAKIIFWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILYGNEDKRF 300  
QY 301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPOPSGNLRPPQSEEEVKHL 360  
Db 301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPOPSGNLRPPQSEEEVKHL 360  
QY 361 GYASHLMEIFCDSEENTEFTSQESLSRTIPPDKTIVIEYDVRTTIDICAGPEEQELS 420  
Db 361 GYASHLMEIFCDSEENTEFTSQESLSRTIPPDKTIVIEYDVRTTIDICAGPEEQELS 420  
QY 421 LQEEVSTQGLLESQAALAVLGPQTLOYSYTPQLQDLPLAQHHTSEEGPSEEPSTTLV 480  
Db 421 LQEEVSTQGLLESQAALAVLGPQTLOYSYTPQLQDLPLAQHHTSEEGPSEEPSTTLV 480  
QY 481 DMDPQTRGLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEAPADPPGGENETVLMQ 540  
Db 481 DMDPQTRGLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEAPADPPGGENETVLMQ 540  
QY 541 FMEEWGLYVQMEN 553  
Db 541 FMEEWGLYVQMEN 553  
RESULT 5  
AAE23353  
ID AAE23353 standard; protein; 553 AA.  
XX AAE23353;  
XX 27-AUG-2002 (first entry)  
XX Human interleukin-20 receptor alpha (IL-20RA) protein.  
XX Human; interleukin-19; IL-19; interleukin-20 receptor alpha; IL-20RA;  
KW interleukin-20 receptor beta; IL-20RB; inflammation; atherosclerosis;  
KW diabetes; reperfusion injury; cancer; infectious meningitis; cataract;  
KW rheumatoid arthritis; rheumatic fever; systemic lupus erythematosus;  
KW antibacterial; cytostatic; dermatological; ophthalmological; vasotropic.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..29 /label= signal\_peptide  
FT Protein 30..553 /note= "Human mature IL-20RA protein"  
XX WO200222153-A2.  
XX 21-MAR-2002.  
XX 13-SEP-2001; 2001WO-US028557.  
XX 15-SEP-2000; 2000US-0233305P.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Chandrasekhar YA, Jaspers SR;  
XX WPI; 2002-425815/45.  
DR N-PSDB; AAD37554.  
XX Method of down-regulating IL-19 useful for treating inflammation  
PT comprises administration of a polypeptide comprised of the extracellular  
PT domain of IL-20RA and IL-20RB.  
XX Disclosure; Page 45-47; 80pp; English.  
PS



XX The present invention relates to a method of down-regulating interleukin  
CC (IL)-19. The method involves administration of a polypeptide comprised of  
CC the extracellular domain of interleukin-20 receptor alpha (IL-20RA). The  
CC the extracellular domain of interleukin-20 receptor beta (IL-20RB). The  
CC IL-20RA and IL-20RB are heterodimeric receptors that bind to both IL-19  
CC and mda7. The method is useful for down-regulating IL-19, useful for the  
CC treatment of inflammation e.g., in diabetes, arteriosclerosis, cataracts,  
CC reperfusion injury, cancer, infectious meningitis, rheumatoid arthritis,  
CC rheumatic fever and systemic lupus erythematosus. The present sequence is  
CC human IL-20RA protein  
XX  
XX Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 5; Length 553;  
Best Local Similarity 100.0%; Pred. No. 5.6e-240;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60  
Db 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60  
QY 61 GLQGVKVTYTVQYFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAINGTKC 120  
Db 61 GLQGVKVTYTVQYFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAINGTKC 120  
QY 121 SKWASGRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQIYSNLK 180  
Db 121 SKWASGRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQIYSNLK 180  
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240  
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240  
QY 241 KQOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDPKRF 300  
Db 241 KQOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDPKRF 300  
QY 301 FVPAEKIVNFTLNISDDSKISHQDMSLLGKSSDVSSNDPQPSGNLRPPQEESEVKHL 360  
Db 301 FVPAEKIVNFTLNISDDSKISHQDMSLLGKSSDVSSNDPQPSGNLRPPQEESEVKHL 360  
QY 361 GYASHLMEIFCDSEENTECTSFTQESLSRTTIPDKTVIEYDVRTTIDICAGPEEQELS 420  
Db 361 GYASHLMEIFCDSEENTECTSFTQESLSRTTIPDKTVIEYDVRTTIDICAGPEEQELS 420  
QY 421 LOEEVSTQGTLLSQALAVLGPQTLYSYTQQLDPLAQHTDSEEGPEEPSTTLV 480  
Db 421 LOEEVSTQGTLLSQALAVLGPQTLYSYTQQLDPLAQHTDSEEGPEEPSTTLV 480  
QY 481 DWDPTGRLCIPSLSSFDQDSECEPSEGDLGEEGLLSRLYEAPADPPGNETYLMQ 540  
Db 481 DWDPTGRLCIPSLSSFDQDSECEPSEGDLGEEGLLSRLYEAPADPPGNETYLMQ 540  
QY 541 FMEEWGLYQMEN 553  
Db 541 FMEEWGLYQMEN 553

RESULT 6  
ABR38943  
ID ABR38943 standard; protein; 553 AA.  
XX  
XX ABR38943;  
AC  
XX  
XX 10-MAY-2003 (first entry)  
DT  
DE Human AK155 receptor alpha subunit # SEQ ID 1.  
DE  
XX AK155 receptor; cytokine receptor; inflammation; Crohn's disease;  
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;  
KW asthma; allergy; diabetes mellitus; Sjogren's syndrome;  
KW transplant rejection; angiogenesis; cancer.

XX Homo sapiens.  
OS  
XX WO2003002717-A2.  
PN  
XX 09-JAN-2003.  
PD  
XX 27-JUN-2002; 2002WO-US020489.  
PF  
XX 28-JUN-2001; 2001US-0302176P.  
PR 03-JAN-2002; 2002US-0345690P.  
XX  
XX (SCHE ) SCHERING CORP.  
PA (FINK/) FINKENSCHER H.  
XX  
XX Finkenschcer H, De Waal Malefyt R, Nagalakshmi ML, Moore K;  
PI  
XX WPI; 2003-278256/27.  
DR N-PSDB; ABZ79509.  
XX  
XX New cells recombinantly altered to express an exogenous AK155 cytokine  
PT receptor, useful for identifying agents for treating AK155-mediated  
PT diseases, e.g. inflammation, angiogenesis or cancer.  
XX  
XX Claim 2; Page 63; 100pp; English.  
XX  
XX The present invention relates to a cell recombinantly altered to express  
CC an exogenous AK155 cytokine receptor comprising alpha and beta subunits.  
CC The cytokine receptor, when expressed in Ba/F3 cells, binds to AK155 and  
CC stimulates binding of STAT3 to interferon (IFN) gamma-activated  
CC sequences. The cell is useful in expressing AK155 cytokine receptor which  
CC may be used for identifying therapeutic agents useful for treating AK155-  
CC mediated conditions or diseases, such as inflammation (e.g. Crohn's  
CC disease), autoimmune diseases (e.g. multiple sclerosis, rheumatoid  
CC arthritis, psoriasis, asthma, allergies, diabetes mellitus, Sjogren's  
CC syndrome), transplant rejection, angiogenesis, and cancer. The current  
CC sequence represents the human AK155 receptor alpha subunit  
XX  
XX Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 6; Length 553;  
Best Local Similarity 100.0%; Pred. No. 5.6e-240;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60  
Db 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60  
QY 61 GLQGVKVTYTVQYFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAINGTKC 120  
Db 61 GLQGVKVTYTVQYFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAINGTKC 120  
QY 121 SKWASGRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQIYSNLK 180  
Db 121 SKWASGRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQIYSNLK 180  
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240  
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240  
QY 241 KQOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDPKRF 300  
Db 241 KQOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDPKRF 300  
QY 301 FVPAEKIVNFTLNISDDSKISHQDMSLLGKSSDVSSNDPQPSGNLRPPQEESEVKHL 360  
Db 301 FVPAEKIVNFTLNISDDSKISHQDMSLLGKSSDVSSNDPQPSGNLRPPQEESEVKHL 360  
QY 361 GYASHLMEIFCDSEENTECTSFTQESLSRTTIPDKTVIEYDVRTTIDICAGPEEQELS 420  
Db 361 GYASHLMEIFCDSEENTECTSFTQESLSRTTIPDKTVIEYDVRTTIDICAGPEEQELS 420  
QY 421 LOEEVSTQGTLLSQALAVLGPQTLYSYTQQLDPLAQHTDSEEGPEEPSTTLV 480

```

Db 421 LQEEVSTQGLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
QY 481 DWDPTGRLCIPSLSSFDQDSECEPSEGGGLGEGLLSRLYEHPADPPGNETYLMQ 540
Db 481 DWDPTGRLCIPSLSSFDQDSECEPSEGGGLGEGLLSRLYEHPADPPGNETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
Db 541 FMEEWGLYVQMEN 553

RESULT 7
ID ABP70950
AC ABP70950 standard; protein; 553 AA.
XX
XX
XX 17-JUL-2003 (first entry)
XX
XX Interleukin-20 receptor 1, IL-20R1.
DE
XX Cytostatic; interleukin-22R1; interleukin-20R2; Mob-5; interleukin-24;
XX interleukin-20R1; IL-22R1; IL-20R2; IL-24; IL-20R1; cancer.
XX
XX Unidentified.
XX
XX WO2003029262-A2.
XX
XX 10-APR-2003.
XX
XX 29-AUG-2002; 2002WO-US028050.
XX
XX 29-AUG-2001; 2001US-0315684P.
XX
XX (UYVA-) UNIV VANDERBILT.
XX
XX Liang P;
XX
XX WPI; 2003-381601/36.
XX
XX N-PSDB; ACC42677.
XX
XX New complexes of Mob-5 (IL-24) receptors, useful for detecting the
XX presence of cancer (e.g. colorectal cancer) in a patient, particularly as
XX markers for the early diagnosis of cancer, or for screening anti-cancer
XX agents.
XX
XX Disclosure; Page 74-75; 76pp; English.
XX
XX The present invention relates to novel compositions comprising complexes
XX between: (a) interleukin (IL)-22R1 and IL-20R2; (b) Mob-5 (IL-24) and IL-
XX 22R1 and IL-20R2; (c) Mob-5 and IL-20R1 and IL-20R2; (d) Mob-5 and IL-
XX 22R1; (e) Mob-5 and IL-20R2; or (f) Mob-5 and IL-20R1. The compositions
XX are useful for detecting the presence of cancer (e.g. a ras-induced
XX cancer or a colorectal cancer) in a patient. The present sequence is IL-
XX 20R1, used in the compositions of the invention
XX
XX Sequence 553 AA;
XX
XX Query Match 100.0%; Score 2947; DB 6; Length 553;
XX Best Local Similarity 100.0%; Pred. No. 5,6e-240;
XX Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MRAPGRPALRPLPLPPLLLLLLAAPMGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
Db 1 MRAPGRPALRPLPLPPLLLLLLAAPMGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
QY 61 GLOGKVTVTVQVFIYGCKWLNKSECRNINRYCDLSAETSDYEHQYAKVAIWGTC 120
Db 61 GLOGKVTVTVQVFIYGCKWLNKSECRNINRYCDLSAETSDYEHQYAKVAIWGTC 120
QY 121 SKWAESGRFPFLETOIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180

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Db 121 SKWAESGRFPFLETOIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
QY 181 YNVSVLNTKSNRTWQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
Db 181 YNVSVLNTKSNRTWQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHYGKEKHPANLILIYGNEDFKRF 300
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHYGKEKHPANLILIYGNEDFKRF 300
QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLPPQSEEEVKHL 360
Db 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLPPQSEEEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQOESLSRTIPPDKTVIEYEDVTRTTDICAGPEQELS 420
Db 361 GYASHLMEIFCDSEENTEGTSFTQOESLSRTIPPDKTVIEYEDVTRTTDICAGPEQELS 420
QY 421 LQEEVSTQGLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
Db 421 LQEEVSTQGLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
QY 481 DWDPTGRLCIPSLSSFDQDSECEPSEGGGLGEGLLSRLYEHPADPPGNETYLMQ 540
Db 481 DWDPTGRLCIPSLSSFDQDSECEPSEGGGLGEGLLSRLYEHPADPPGNETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
Db 541 FMEEWGLYVQMEN 553

RESULT 8
ADJ83291
ID ADJ83291 standard; protein; 553 AA.
XX
XX ADJ83291;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human interleukin receptor IL-20RA subunit full-length protein.
XX
XX inflammation; single chain antibody; interleukin; IL-20; IL-20RA subunit;
XX IL-20RB subunit; antiinflammatory; dermatological; antipsoriatic;
XX antiarthritic; respiratory; antiasthmatic; antiulcer; antibacterial;
XX immunosuppressive; gastrointestinal; skin; psoriasis; eczema;
XX atopic dermatitis; contact dermatitis; lung;
XX adult respiratory distress syndrome; asthma; bronchitis; pneumonia;
XX arthritis; septic shock; multiple organ failure; bowel;
XX ulcerative colitis; Crohn's disease; human; receptor.
XX
XX Homo sapiens.
XX
XX US2004005320-A1.
XX
XX 08-JAN-2004.
XX
XX 28-APR-2003; 2003US-00424658.
XX
XX 23-DEC-1999; 99US-0171969P.
XX
XX 22-JUN-2000; 2000US-0213341P.
XX
XX 22-DEC-2000; 2000US-00746359.
XX
XX (THOM/) THOMPSON P.
XX (FOST/) FOSTER D C.
XX (XUWW/) XU W.
XX (MADD/) MADDEN K L.
XX (KELL/) KELLY J D.
XX (SPRE/) SPRECHER C A.
XX (BLUM/) BLUMBERG H.
XX (EAGA/) EAGAN M A.
XX (JASP/) JASPERS S R.
XX (CHAN/) CHANDRASEKHAR Y A.
XX (NOVA/) NOVAK J E.

```

XX Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA;  
PI Blumberg H, Bagan MA, Jaspers SR, Chandrasekhar YA, Novak JE;  
XX N-PSDB; ADJ83290.  
XX WPI; 2004-081696/08.  
XX Reducing or treating inflammation, e.g. inflammatory lung disease,  
PT comprises administering an antibody, antibody fragment or single chain  
PT antibody that specifically binds to an interleukin (IL)-20RA subunit of  
PT an IL-20 receptor.  
XX Example 5; SEQ ID NO 11; 69pp; English.  
XX The invention relates to a novel method of reducing or treating  
CC inflammation in a mammal which comprises administering an antibody,  
CC antibody fragment or single chain antibody which specifically binds to a  
CC receptor of interleukin (IL)-20 comprising an IL-20RA subunit and an IL-  
CC 20RB subunit. The method of the invention has antiinflammatory,  
CC dermatological, antipruritic, antiarthritic, respiratory, antiasthmatic,  
CC antitumor, antibacterial, immunosuppressive and gastrointestinal  
CC applications and may be useful for reducing or treating an inflammation,  
CC including an inflammatory skin disease such as psoriasis, eczema, atopic  
CC dermatitis and contact dermatitis or an inflammatory lung disease such as  
CC adult respiratory distress syndrome, asthma, bronchitis and pneumonia, as  
CC well as arthritis, septic shock, multiple organ failure, inflammatory  
CC bowel disease, ulcerative colitis or Crohn's disease. The current  
CC invention is that of the human IL-20RA subunit-related protein of the  
CC invention.  
XX Sequence 553 AA;  
SQ  
Query Match 100.0%; Score 2947; DB 8; Length 553;  
Best Local Similarity 100.0%; Pred. No. 5.6e-240;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRAPGRPALRPLPPLLLILLALPAGRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60  
DB 1 MRAPGRPALRPLPPLLLILLALPAGRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60  
QY 61 GLOGVKTVTYQVFIYGQKWLKNSCRNINRYCDLSAETSDYEHQYAKVKAIWGTC 120  
DB 61 GLOGVKTVTYQVFIYGQKWLKNSCRNINRYCDLSAETSDYEHQYAKVKAIWGTC 120  
QY 121 SKWAESGRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQOIYSNLK 180  
DB 121 SKWAESGRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQOIYSNLK 180  
QY 181 YNVSVLNTKSNRTWSQCVNHTLVLTWLEPNTLYCVHVESFVGPFPRAQPSKQCARTL 240  
DB 181 YNVSVLNTKSNRTWSQCVNHTLVLTWLEPNTLYCVHVESFVGPFPRAQPSKQCARTL 240  
QY 241 KDQSSRFKAKIIFWYVLPTISITVFLFSVMGYSIYRIHVGEKHPANLILYNEFDKRF 300  
DB 241 KDQSSRFKAKIIFWYVLPTISITVFLFSVMGYSIYRIHVGEKHPANLILYNEFDKRF 300  
QY 301 FVPAEKIVINFITLINSDDSKISHQDMSLLGKSSDVSSSLNDPQPSGNLRPPQEEVKGHL 360  
DB 301 FVPAEKIVINFITLINSDDSKISHQDMSLLGKSSDVSSSLNDPQPSGNLRPPQEEVKGHL 360  
QY 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPDKTVIIEYDVRTTDCAGPESQELS 420  
DB 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPDKTVIIEYDVRTTDCAGPESQELS 420  
QY 421 LOBEVSTQGLTLLSQALAVLGQTQYVTPQLQDLPLAQSHRTDSEGPPEPSTTLV 480  
DB 421 LOBEVSTQGLTLLSQALAVLGQTQYVTPQLQDLPLAQSHRTDSEGPPEPSTTLV 480  
QY 481 DWDPTQGRLCIPSLSSPDQSEGCSEPGDGLGEGLLSLYEAPAPDRPPGNETYLMQ 540  
DB 481 DWDPTQGRLCIPSLSSPDQSEGCSEPGDGLGEGLLSLYEAPAPDRPPGNETYLMQ 540  
QY 541 FMEEWGLYVQMEN 553

Db 541 FMEEWGLYVQMEN 553  
RESULT 9  
ADJ75638  
ID ADJ75638 standard; protein; 553 AA.  
XX ADJ75638;  
AC ADJ75638;  
XX 20-MAY-2004 (first entry)  
DT 20-MAY-2004 (first entry)  
XX Marker gene related amino acid sequence SEQ ID NO:890.  
XX bronchial asthma; chronic obstructive pulmonary disease;  
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
KW gene therapy; marker.  
XX Homo sapiens.  
XX EP1394274-A2.  
XX 03-MAR-2004.  
XX 04-AUG-2003; 2003EP-00254857.  
XX 06-AUG-2002; 2002JP-00229312.  
PR 20-MAR-2003; 2003JP-00077212.  
XX (GENO-) GENOX RES INC.  
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;  
XX WPI; 2004-193155/19.  
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by  
PT comparing the expression level of a marker gene in a biological sample  
PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.  
XX Example 11; SEQ ID NO 890; 241pp; English.  
XX The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic  
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
CC genes (S1) whose expression levels increase when respiratory epithelial  
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
CC whose expression levels decrease when respiratory epithelial cells are  
CC stimulated with interleukin-13. Also described: (1) a reagent (1) for  
CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
CC (2) a kit for screening for a candidate compound for a therapeutic agent  
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
CC an animal model for bronchial asthma or chronic obstructive pulmonary  
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
CC method for producing an animal model for bronchial asthma or chronic  
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
CC a marker gene or an antisense nucleic acid corresponding to a portion of  
CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
CC expression of the gene through an RNAi effect or an antibody recognizing  
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
CC probe has been immobilized to assay a marker gene. (I) has respiratory  
CC and antiasthmatic activities, and can be used in gene therapy. The method  
CC is useful for testing for or screening for a therapeutic agent for  
CC bronchial asthma or chronic obstructive pulmonary disease. The present  
CC sequence is used in the exemplification of the present invention.  
XX Sequence 553 AA;  
SQ

Query Match		100.0%; Score 2947; DB 8; Length 553;
Best Local Similarity		100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
DB	1	MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
QY	61	GLQGVKVTYVQVFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
DB	61	GLQGVKVTYVQVFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
QY	121	SKWAESGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYSNLK 180
DB	121	SKWAESGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYSNLK 180
QY	181	YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVSEFVPGPPRRAQPSKQCARTL 240
DB	181	YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVSEFVPGPPRRAQPSKQCARTL 240
QY	241	KQOSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILIIYGNFDFKRF 300
DB	241	KQOSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILIIYGNFDFKRF 300
QY	301	FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQBESEVKHL 360
DB	301	FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQBESEVKHL 360
QY	361	GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTIDICAGPEEQELS 420
DB	361	GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTIDICAGPEEQELS 420
QY	421	LOBEVSTQGTLLSQALAVLGPQTLYSYTTPQLQDLPLAQHSTDSEEGPEEPSTTLV 480
DB	421	LOBEVSTQGTLLSQALAVLGPQTLYSYTTPQLQDLPLAQHSTDSEEGPEEPSTTLV 480
QY	481	DWDPTQGRLCIPSLSSFDQDSECEPSEGDLGEGLLSRLYEEDPADRPPGENETVLMQ 540
DB	481	DWDPTQGRLCIPSLSSFDQDSECEPSEGDLGEGLLSRLYEEDPADRPPGENETVLMQ 540
QY	541	FMEEWGLYQMEN 553
DB	541	FMEEWGLYQMEN 553
RESULT 11		
ADW64528		
ID	ADW64528	standard; protein; 553 AA.
XX	XX	
AC	ADW64528;	
XX	XX	
DT	24-MAR-2005	(first entry)
XX	XX	
DE	Human IL-20RA protein.	
XX	XX	
KW	Therapy; cns-gen.; respiratory-gen.; antiasthmatic; antipsoriatic;	

Query Match		100.0%; Score 2947; DB 8; Length 553;
Best Local Similarity		100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
DB	1	MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
QY	61	GLQGVKVTYVQVFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
DB	61	GLQGVKVTYVQVFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
QY	121	SKWAESGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYSNLK 180
DB	121	SKWAESGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYSNLK 180
QY	181	YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVSEFVPGPPRRAQPSKQCARTL 240
DB	181	YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVSEFVPGPPRRAQPSKQCARTL 240
QY	241	KQOSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILIIYGNFDFKRF 300
DB	241	KQOSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILIIYGNFDFKRF 300
QY	301	FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQBESEVKHL 360
DB	301	FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQBESEVKHL 360
QY	361	GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTIDICAGPEEQELS 420
DB	361	GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTIDICAGPEEQELS 420
QY	421	LOBEVSTQGTLLSQALAVLGPQTLYSYTTPQLQDLPLAQHSTDSEEGPEEPSTTLV 480
DB	421	LOBEVSTQGTLLSQALAVLGPQTLYSYTTPQLQDLPLAQHSTDSEEGPEEPSTTLV 480
QY	481	DWDPTQGRLCIPSLSSFDQDSECEPSEGDLGEGLLSRLYEEDPADRPPGENETVLMQ 540
DB	481	DWDPTQGRLCIPSLSSFDQDSECEPSEGDLGEGLLSRLYEEDPADRPPGENETVLMQ 540
QY	541	FMEEWGLYQMEN 553
DB	541	FMEEWGLYQMEN 553
RESULT 10		
ADN04874		
XX	ADN04874	standard; protein; 553 AA.
AC	ADN04874;	
XX	XX	
DT	01-JUL-2004	(first entry)
XX	XX	
DE	Antipsoriatic protein sequence #617.	
DE	antipsoriatic; gene therapy; psoriasis; diagnosis.	
KW	Homo sapiens.	
OS	Wo2004028479-A2.	
PN	08-APR-2004.	
XX	XX	
PF	25-SEP-2003; 2003WO-US030907.	
XX	XX	
PR	25-SEP-2002; 2002US-0414006P.	
XX	XX	
PA	(GETH ) GENENTECH INC.	
XX	XX	
PI	Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;	
PI	Wu TD;	
XX	XX	

KW	antiinflammatory; psoriasis; dermatological disease; immune disorder;	301	FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDDPQPSGNLRPPQEEEVKHL	360
KW	pulmonary disease; asthma; inflammation; respiratory disease; bronchitis;	361	GYASHLWEIFCDSEENTECTSFTQESLSRTIIPDKTVIEYVDVTRTDDICAGPEOEELS	420
KW	antiinflammatory; inflammation; cystic fibrosis;	361	GYASHLWEIFCDSEENTECTSFTQESLSRTIIPDKTVIEYVDVTRTDDICAGPEOEELS	420
KW	gastrointestinal disease; chemotherapy; interleukin.	421	LQEEVSTQGTLLSQALAVLGPQTTLQYSYTPQLDPLAQHHTDSEEGPEEPSTTLV	480
XX	Homo sapiens.	421	LQEEVSTQGTLLSQALAVLGPQTTLQYSYTPQLDPLAQHHTDSEEGPEEPSTTLV	480
XX	US2005003475-A1.	481	DWDPTGRLCIPSLSSFDQDSECGCEPSEGDLGEGLLSRLYBEPAPDRPPGNETYLMQ	540
XX	06-JAN-2005.	481	DWDPTGRLCIPSLSSFDQDSECGCEPSEGDLGEGLLSRLYBEPAPDRPPGNETYLMQ	540
XX	22-DEC-2000; 2000US-00745792.	541	FMEEWGLYVQMEN 553	
XX	23-DEC-1999; 99US-0171966P.	541	FMEEWGLYVQMEN 553	
XX	22-JUN-2000; 2000US-0213416P.			
XX	(POST/) FOSTER D C.			
PA	(XUWV/) XU W.			
PA	(MADD/) MADDEN K L.			
PA	(KELL/) KELLY J D.			
PA	(SPRE/) SPRECHER C A.			
PA	(BRAN/) BRANDT C S.			
PA	(RIXO/) RIXON M W.			
PA	(PRES/) PRESNELL S R.			
PA	(FOX/) FOX B A.			
XX	Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;			
PI	Rixon MW, Presnell SR, Fox BA;			
XX	WPI; 2005-065240/07.			
DR	N-PSDB; ADW64527.			
XX				
XX	New isolated soluble receptor comprised of an interleukin 20 receptor			
PT	alpha (IL-20RA) subunit and a IL-20RB subunit, useful for treating			
PT	inflammatory diseases e.g., psoriasis and inflammatory lung diseases			
PT	e.g., asthma.			
XX				
PS	Example 5; SEQ ID NO 11; 73pp; English.			
XX				
CC	The present invention relates to a soluble receptor having an			
CC	interleukin 20 receptor alpha (IL-20RA) subunit and an IL-20RB subunit.			
CC	The invention is useful for treating inflammatory diseases such as			
CC	psoriasis and inflammatory lung diseases such as asthma, bronchitis and			
CC	cystic fibrosis. The present sequence is the human IL-20RA protein.			
XX				
XX	Sequence 553 AA;			
XX				
XX	Query Match 100.0%; Score 2947; DB 9; Length 553;			
XX	Best Local Similarity 100.0%; Pred. No. 5.6e-240;			
XX	Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 MRAPGRPALRPLPLPPLLLLLAALPGRAPVPCVSGGLPKPANITPLSINMKNVLTQTPPE	60		
DB	1 MRAPGRPALRPLPLPPLLLLLAALPGRAPVPCVSGGLPKPANITPLSINMKNVLTQTPPE	60		
QY	61 GLOGVKVTYVQYFIYQCKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAINGTKC	120		
DB	61 GLOGVKVTYVQYFIYQCKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAINGTKC	120		
QY	121 SKWASGRFYPPFLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPDLFVSMQOIYSNLK	180		
DB	121 SKWASGRFYPPFLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPDLFVSMQOIYSNLK	180		
QY	181 YNVSVLNTKSNRTWSQVNTHTLVLTWLEPNTLYCVHVESFVPGPRRAQPSKQCARTL	240		
DB	181 YNVSVLNTKSNRTWSQVNTHTLVLTWLEPNTLYCVHVESFVPGPRRAQPSKQCARTL	240		
QY	241 KQSSFEKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDKRP	300		
DB	241 KQSSFEKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDKRP	300		
QY	301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDDPQPSGNLRPPQEEEVKHL	360		
DB	301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDDPQPSGNLRPPQEEEVKHL	360		
DB	361 GYASHLWEIFCDSEENTECTSFTQESLSRTIIPDKTVIEYVDVTRTDDICAGPEOEELS	420		
DB	361 GYASHLWEIFCDSEENTECTSFTQESLSRTIIPDKTVIEYVDVTRTDDICAGPEOEELS	420		
QY	421 LQEEVSTQGTLLSQALAVLGPQTTLQYSYTPQLDPLAQHHTDSEEGPEEPSTTLV	480		
DB	421 LQEEVSTQGTLLSQALAVLGPQTTLQYSYTPQLDPLAQHHTDSEEGPEEPSTTLV	480		
QY	481 DWDPTGRLCIPSLSSFDQDSECGCEPSEGDLGEGLLSRLYBEPAPDRPPGNETYLMQ	540		
DB	481 DWDPTGRLCIPSLSSFDQDSECGCEPSEGDLGEGLLSRLYBEPAPDRPPGNETYLMQ	540		
QY	541 FMEEWGLYVQMEN 553			
DB	541 FMEEWGLYVQMEN 553			
DB	RESULT 12			
DB	AEA50101			
ID	AEA50101 standard; protein; 553 AA.			
XX	AC			
XX	AEA50101;			
XX	AC			
DT	11-AUG-2005 (first entry)			
XX	Mouse IL-20RA.			
XX	Antiinflammatory; Gastrointestinal-Gen.; Antulcer; Antiarthritic;			
KW	Dermatological; Antipsoriatic; Antibacterial; Immunosuppressive;			
KW	Antimicrobial; IL-Antagonist-20; interleukin-20; IL-20; inflammation;			
KW	Inflammatory bowel disease; ulcerative colitis; Crohns disease;			
KW	arthritis; atopic dermatitis; psoriasis; endotoxemia; septicemia;			
KW	toxic shock syndrome; infectious disease; expressed sequence tag.			
XX				
OS	Mus sp.			
OS	Synthetic.			
XX				
PN	WO2005052000-A2.			
XX				
PD	09-JUN-2005.			
XX				
PF	19-NOV-2004; 2004WO-US039071.			
XX				
PR	21-NOV-2003; 2003US-0524131P.			
PR	24-MAR-2004; 2004US-0555857P.			
XX				
PA	(ZYMO ) ZYMOGENETICS INC.			
XX				
PI	Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekher YA;			
PI	Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;			
XX				
DR	WPI; 2005-4053359/41.			
XX	N-PSDB; AEA50102.			
XX				
PT	Producing an antibody to an interleukin-20 (IL-20) polypeptide, useful			
PT	for treating inflammatory diseases e.g., Crohn's disease, by inoculating			
PT	an animal with the polypeptide eliciting an immune response to produce			
PT	the antibody.			
XX				
PS	Example 2; SEQ ID NO 54; 268pp; English.			
XX				
CC	This sequence represents murine interleukin-20RA (IL-20RA). The method of			
CC	the invention for producing an antibody to IL-20 comprises inoculating an			
CC	animal with an IL-20 polypeptide which elicits an immune response in the			
CC	animal to produce the antibody, and isolating the antibody from the			
CC	animal. The antibody is useful for treating a pathological condition in a			
CC	subject associated with IL-20 activity such as chronic inflammatory			
CC	condition, specifically inflammatory bowel disease, ulcerative colitis,			
CC	Crohns' disease, arthritis, atopic dermatitis and psoriasis, or acute			
CC	inflammatory condition such as endotoxemia, septicemia, toxic shock			
CC	syndrome and infectious disease. An antagonist of IL-20 is useful for			

CC treating a mammal afflicted with an inflammatory disease in which IL-20  
CC plays a role such that the inflammation is reduced, where the antagonist  
CC comprises an antibody, antibody fragment, or binding polypeptide that  
CC specifically binds a polypeptide or polypeptide fragment of IL-20 or a  
CC polypeptide or polypeptide fragment of IL-20, and where the inflammatory  
CC activity of IL-20 is reduced. The method is useful for producing such  
CC therapeutic antibody. The antibody or antibody fragment, produced using  
CC the above method, binds to IL-20, and inhibits or reduces the pro-  
CC inflammatory activity of IL-20. IL-20-induced proliferation or  
CC differentiation of hematopoietic cells and hematopoietic cell progenitors  
CC may be reduced or inhibited using the antibody.  
XX  
SQ Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 9; Length 553;  
Best Local Similarity 100.0%; Pred. No. 5.6e-240;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60  
DB 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60  
QY 61 GLQGVKVTYVQYFYIGQKKWLNSKRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120  
DB 61 GLQGVKVTYVQYFYIGQKKWLNSKRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120  
QY 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPKWKKNPDLPVSMQOIYSNLK 180  
DB 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPKWKKNPDLPVSMQOIYSNLK 180  
QY 181 YNVSVLNTKSNRTWSCVNTNHTLVLTWLEPNTLYCVHVESFVGGPPRRAPQSEKQCARTL 240  
DB 181 YNVSVLNTKSNRTWSCVNTNHTLVLTWLEPNTLYCVHVESFVGGPPRRAPQSEKQCARTL 240  
QY 241 KQSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILYGNFDPKRP 300  
DB 241 KQSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILYGNFDPKRP 300  
QY 301 FYPAEKIVNFIPLNTSDPSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEERVKHL 360  
DB 301 FYPAEKIVNFIPLNTSDPSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEERVKHL 360  
QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYEDVTRTIDICAGPEQEELS 420  
DB 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYEDVTRTIDICAGPEQEELS 420  
QY 421 LQEEVSTQGTLLSQALAVLGQTLQYVTPQLQDLPLAQHHTDSBEGPBEETTLV 480  
DB 421 LQEEVSTQGTLLSQALAVLGQTLQYVTPQLQDLPLAQHHTDSBEGPBEETTLV 480  
QY 481 DWDPTGRLCIPLSLSDQDSECEPSEGGDLGEGLLSRLVEEAPDRPPGENETYLMO 540  
DB 481 DWDPTGRLCIPLSLSDQDSECEPSEGGDLGEGLLSRLVEEAPDRPPGENETYLMO 540  
QY 541 FMEEWGLYVQMEN 553  
DB 541 FMEEWGLYVQMEN 553

RESULT 13  
AEA50061  
ID AEA50061 standard; protein; 553 AA.  
XX  
AC AEA50061;  
XX  
XX 11-AUG-2005 (first entry)  
XX Human IL-20RA extracellular domain.  
XX Antinflammatory; Gastrointestinal-Gen.; Antiulcer; Antiarthritic;  
KW Dermatological; Antipsoriatic; Antibacterial; Immunosuppressive;  
KW Antimicrobial; IL-Antagonist-20; interleukin-20; IL-20; inflammation;  
KW inflammatory bowel disease; ulcerative colitis; Crohns disease;

KW arthritis; atopic dermatitis; psoriasis; endotoxemia; septicemia;  
KW toxic shock syndrome; infectious disease.  
XX  
OS Homo sapiens.  
XX Synthetic.  
PN WO2005052000-A2.  
XX  
PD 09-JUN-2005.  
XX  
PF 19-NOV-2004; 2004WO-US039071.  
XX  
PR 21-NOV-2003; 2003US-0524131P.  
PR 24-MAR-2004; 2004US-0555857P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekher YA;  
PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;  
XX  
XX WPI: 2005-405359/41.  
DR N-PSDB; AEA50060.  
XX  
PT Producing an antibody to an interleukin-20 (IL-20) polypeptide, useful  
PT for treating inflammatory diseases e.g., Crohn's disease, by inoculating  
PT an animal with the polypeptide eliciting an immune response to produce  
PT the antibody.  
XX  
PS Example 7; SEQ ID NO 14; 268pp; English.  
XX

CC This sequence represents the human interleukin-20RA (IL-20RA)  
CC extracellular domain which was used generation of a human IL-20RA  
CC extracellular domain immunoglobulin gamma 1 heavy chain constant region  
CC fusion construct. The method of the invention for producing an antibody  
CC to IL-20 comprises inoculating an animal with an IL-20 polypeptide which  
CC elicits an immune response in the animal to produce the antibody, and  
CC isolating the antibody from the animal. The antibody is useful for  
CC treating a pathological condition in a subject associated with IL-20  
CC activity such as chronic inflammatory condition, specifically  
CC inflammatory bowel disease, ulcerative colitis, Crohns' disease,  
CC arthritis, atopic dermatitis and psoriasis, or acute inflammatory  
CC condition such as endotoxemia, septicemia, toxic shock syndrome and  
CC infectious disease. An antagonist of IL-20 is useful for treating a  
CC mammal afflicted with an inflammatory disease in which IL-20 plays a role  
CC such that the inflammation is reduced, where the antagonist comprises an  
CC antibody, antibody fragment, or binding polypeptide that specifically  
CC binds a polypeptide or polypeptide fragment of IL-20 or a polypeptide or  
CC polypeptide fragment of IL-20, and where the inflammatory activity of IL-  
CC 20 is reduced. The method is useful for producing such therapeutic  
CC antibody. The antibody or antibody fragment, produced using the above  
CC method, binds to IL-20, and inhibits or reduces the pro-inflammatory  
CC activity of IL-20. IL-20-induced proliferation or differentiation of  
CC hematopoietic cells and hematopoietic cell progenitors may be reduced or  
CC inhibited using the antibody.

Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 9; Length 553;  
Best Local Similarity 100.0%; Pred. No. 5.6e-240;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60  
DB 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60  
QY 61 GLQGVKVTYVQYFYIGQKKWLNSKRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120  
DB 61 GLQGVKVTYVQYFYIGQKKWLNSKRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120  
QY 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPKWKKNPDLPVSMQOIYSNLK 180  
DB 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPKWKKNPDLPVSMQOIYSNLK 180

QY 181 YNVSVLNTRKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVGPSPRRAPQSEKQCARTL 240  
 Db |||||||  
 QY 181 YNVSVLNTRKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVGPSPRRAPQSEKQCARTL 240  
 Db |||||||  
 QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVHGEKHPANLILYGNEDKRF 300  
 Db |||||||  
 QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVHGEKHPANLILYGNEDKRF 300  
 Db |||||||  
 QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRAPPQSEEVKHL 360  
 Db |||||||  
 QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRAPPQSEEVKHL 360  
 Db |||||||  
 QY 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVRTTIDICAGPEQELS 420  
 Db |||||||  
 QY 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVRTTIDICAGPEQELS 420  
 Db |||||||  
 QY 421 LQEEVSTQGTLLSQALAVLGPQTLYSYTPOQLDPLAQHSDTSEEGPEEPSTTLV 480  
 Db |||||||  
 QY 421 LQEEVSTQGTLLSQALAVLGPQTLYSYTPOQLDPLAQHSDTSEEGPEEPSTTLV 480  
 Db |||||||  
 QY 481 DWDPTQGLRCLIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPPPGENETVLMQ 540  
 Db |||||||  
 QY 481 DWDPTQGLRCLIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPPPGENETVLMQ 540  
 Db |||||||  
 QY 541 FMEEWGLYVQMEN 553  
 Db |||||||  
 QY 541 FMEEWGLYVQMEN 553  
 Db |||||||

RESULT 14  
 ID AEA50099 standard; protein; 553 AA.  
 AC AEA50099;  
 DT 11-AUG-2005 (first entry)  
 XX Mouse IL-20RA.  
 DE  
 XX Antinflammatory; Gastrointestinal-Gen.; Anticancer; Antiarthritic;  
 KW Dermatological; Antiparasitic; Antibacterial; Immunosuppressive;  
 KW Antimicrobial; IL-Antagonist-20; interleukin-20; IL-20; inflammation;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW arthritis; atopic dermatitis; psoriasis; endotoxemia; septicemia;  
 KW toxic shock syndrome; infectious disease; expressed sequence tag.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX WO2005052000-A2.  
 XX  
 XX 09-JUN-2005.  
 XX  
 XX 19-NOV-2004; 2004WO-US039071.  
 XX  
 XX 21-NOV-2003; 2003US-0524131P.  
 XX 24-MAR-2004; 2004US-0555857P.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Xu W, Kindevogel WR, Chen Z, Hughes SD, Chandrasekhar YA;  
 PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;  
 XX WPI: 2005-405359/41.  
 DR N-PSDB; AEA50100.  
 XX  
 XX Producing an antibody to an interleukin-20 (IL-20) polypeptide, useful  
 PT for treating inflammatory diseases e.g., Crohn's disease, by inoculating  
 PT an animal with the polypeptide eliciting an immune response to produce  
 PT the antibody.  
 XX  
 XX Example 2; SEQ ID NO 52; 268pp; English.

XX

RESULT 15

CC This sequence represents murine interleukin-20RA (IL-20RA). The method of  
 CC the invention for producing an antibody to IL-20 comprises inoculating an  
 CC animal with an IL-20 polypeptide which elicits an immune response in the  
 CC animal to produce the antibody, and isolating the antibody from the  
 CC animal. The antibody is useful for treating a pathological condition in a  
 CC subject associated with IL-20 activity such as chronic inflammatory  
 CC condition, specifically inflammatory bowel disease, ulcerative colitis,  
 CC Crohn's disease, arthritis, atopic dermatitis and psoriasis, or acute  
 CC inflammatory condition such as endotoxemia, septicemia, toxic shock  
 CC syndrome and infectious disease. An antagonist of IL-20 is useful for  
 CC treating a mammal afflicted with an inflammatory disease in which IL-20  
 CC plays a role such that the inflammation is reduced, where the antagonist  
 CC comprises an antibody, antibody fragment, or binding polypeptide that  
 CC specifically binds a polypeptide or polypeptide fragment of IL-20 or a  
 CC polypeptide or polypeptide fragment of IL-20, and where the inflammatory  
 CC activity of IL-20 is reduced. The method is useful for producing such  
 CC therapeutic antibody. The antibody or antibody fragment, produced using  
 CC the above method, binds to IL-20, and inhibits or reduces the pro-  
 CC inflammatory activity of IL-20. IL-20-induced proliferation or  
 CC differentiation of hematopoietic cells and hematopoietic cell progenitors  
 CC may be reduced or inhibited using the antibody. Note: The specification  
 CC refers to Seq ID 52 as being a primer from the 5' UTR of full length  
 CC mouse IL-20RA used to generate the full length sequence. The sequence  
 CC published is actually a duplicate of AEA50101 which is murine IL-20RA.

XX Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 9; Length 553;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-240;  
 Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRAPGRPALRPLPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
 Db |||||||  
 QY 1 MRAPGRPALRPLPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
 Db |||||||

QY 61 GLQGVKVTYTVQYFIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120  
 Db |||||||  
 QY 61 GLQGVKVTYTVQYFIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120  
 Db |||||||

QY 121 SKWASGRFYFPLETOIGPPEVALTTDEKSIISVLTAPEKWKKNPEDLPVSMQOIVSNLK 180  
 Db |||||||  
 QY 121 SKWASGRFYFPLETOIGPPEVALTTDEKSIISVLTAPEKWKKNPEDLPVSMQOIVSNLK 180  
 Db |||||||

QY 181 YNVSVLNTRKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVGPSPRRAPQSEKQCARTL 240  
 Db |||||||  
 QY 181 YNVSVLNTRKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVGPSPRRAPQSEKQCARTL 240  
 Db |||||||

QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVHGEKHPANLILYGNEDKRF 300  
 Db |||||||  
 QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVHGEKHPANLILYGNEDKRF 300  
 Db |||||||

QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRAPPQSEEVKHL 360  
 Db |||||||  
 QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRAPPQSEEVKHL 360  
 Db |||||||

QY 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVRTTIDICAGPEQELS 420  
 Db |||||||  
 QY 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVRTTIDICAGPEQELS 420  
 Db |||||||

QY 421 LQEEVSTQGTLLSQALAVLGPQTLYSYTPOQLDPLAQHSDTSEEGPEEPSTTLV 480  
 Db |||||||  
 QY 421 LQEEVSTQGTLLSQALAVLGPQTLYSYTPOQLDPLAQHSDTSEEGPEEPSTTLV 480  
 Db |||||||

QY 481 DWDPTQGLRCLIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPPPGENETVLMQ 540  
 Db |||||||  
 QY 481 DWDPTQGLRCLIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPPPGENETVLMQ 540  
 Db |||||||

QY 541 FMEEWGLYVQMEN 553  
 Db |||||||  
 QY 541 FMEEWGLYVQMEN 553  
 Db |||||||

XX





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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:41:13 ; Search time 24.1169 Seconds  
(without alignments)  
1066.146 Million cell updates/sec

Title: US-09-745-792A-14  
Perfect score: 1644  
Sequence: 1 MQFTFWLSEIWTSLFMWFF.....VDACATVMSPELLRAWIS 311

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/6 COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/H COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfilees1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1644	100.0	311	2	US-09-746-359A-14
2	1644	100.0	311	2	US-09-991-181-183
3	1644	100.0	311	2	US-09-999-833A-352
4	1644	100.0	311	2	US-09-990-444-183
5	1644	100.0	311	2	US-09-997-333-183
6	1644	100.0	311	2	US-09-992-598-183
7	1644	100.0	311	2	US-10-020-445A-352
8	1620	98.5	311	2	US-09-265-540B-2
9	1477	89.8	301	2	US-09-746-359A-19
10	1234.5	75.1	336	2	US-09-746-359A-57
11	1218	74.1	239	2	US-10-233-873A-2
12	1209	73.5	352	2	US-09-746-359A-21
13	1080	65.7	203	2	US-09-746-359A-15
14	1075.5	65.4	307	2	US-09-746-359A-58
15	1069	65.0	201	2	US-09-746-359A-59
16	1061	64.5	203	2	US-09-746-359A-68
17	1050	63.9	201	2	US-09-746-359A-61
18	1050	63.9	323	2	US-09-746-359A-60
19	1046	63.6	196	2	US-09-746-359A-67
20	1027	62.5	196	2	US-09-746-359A-69
21	718	43.7	135	2	US-09-746-359A-70
22	699	42.5	135	2	US-09-746-359A-71
23	529	32.2	100	2	US-09-513-999C-7690
24	204	12.4	273	2	US-09-949-016-11056
25	204	12.4	325	1	US-08-683-743-4
26	204	12.4	325	1	US-09-870-574-3
27	204	12.4	325	2	US-09-265-540B-6

28	189.5	11.5	337	2	US-08-871-572B-1	Sequence 1, Appli
29	189.5	11.5	516	2	US-09-949-002-547	Sequence 547, App
30	188.5	11.5	337	2	US-08-871-572B-4	Sequence 4, Appli
31	188.5	11.5	337	2	US-09-265-540B-5	Sequence 5, Appli
32	188.5	11.5	337	2	US-09-949-002-383	Sequence 383, App
33	186.5	11.3	337	4	PCT-US94-14277-8	Sequence 8, Appli
34	184	11.2	258	2	US-08-871-572B-5	Sequence 5, Appli
35	174.5	10.6	557	2	US-07-971-834-4	Sequence 4, Appli
36	173.5	10.6	557	1	US-08-328-256-10	Sequence 10, Appli
37	173.5	10.6	557	1	US-08-471-454-2	Sequence 2, Appli
38	173.5	10.6	557	1	US-08-466-974-2	Sequence 2, Appli
39	173.5	10.6	557	1	US-08-471-453-2	Sequence 2, Appli
40	173.5	10.6	557	1	US-08-307-588-4	Sequence 4, Appli
41	173.5	10.6	557	2	US-09-240-675-4	Sequence 4, Appli
42	173.5	10.6	557	2	US-09-949-016-5972	Sequence 5972, Ap
43	173.5	10.6	575	2	US-09-949-016-8640	Sequence 8640, Ap
44	168	10.2	233	2	US-08-871-572B-8	Sequence 8, Appli
45	164.5	10.0	210	2	US-10-090-365-13	Sequence 13, Appli

## ALIGNMENTS

RESULT 1  
US-09-746-359A-14  
; Sequence 14, Application US/09746359A  
; Patent No. 6610286  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Eagan, Maribeth A.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Chandrasekhar, Yasmin A.  
; APPLICANT: No. 6610286ak, Julia E.  
; TITLE OF INVENTION: Method for Treating Inflammation  
; FILE REFERENCE: 99-108  
; CURRENT APPLICATION NUMBER: US/09/746,359A  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 311  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-746-359A-14

Query Match	100.0%	Score 1644;	DB 2;	Length 311;
Best Local Similarity	100.0%;	Pred. No. 1.8e-165;		
Matches 311;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MQFTFWLSEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLSTNMKHLWMSPVIAP	60	
Db	1	MQFTFWLSEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLSTNMKHLWMSPVIAP	60	
QY	61	GETTVYSVEYQGEYESLYTSHIWPSSWCSLSTEGPCDVTDDITATVPYNLRVATLGSQ	120	
Db	61	GETTVYSVEYQGEYESLYTSHIWPSSWCSLSTEGPCDVTDDITATVPYNLRVATLGSQ	120	
QY	121	TSAWSILKHPFNRSNTILTRPGMEITKOGFHLVIELEDLGPQEFVLVAYWRPPGAEEHV	180	
Db	121	TSAWSILKHPFNRSNTILTRPGMEITKOGFHLVIELEDLGPQEFVLVAYWRPPGAEEHV	180	
QY	181	KMVRSGGIPVHLETPGGAAYCKAOTFYKATGRYSASFQTCVEVOGEAIPLVLTALFAF	240	

Db 181 KMVRSGGIPVHLETFEFGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPVLALFAF 240  
; PRIOR APPLICATION NUMBER: 60/088021  
; PRIOR FILING DATE: 1998-06-04  
Qy 241 VGFMLILVVVPLFVKWGRLLQYSCCPVVVLPTLKITNSPKLISCRSEVDACATAYM 300  
; PRIOR APPLICATION NUMBER: 60/088025  
; PRIOR FILING DATE: 1998-06-04  
Db 241 VGFMLILVVVPLFVKWGRLLQYSCCPVVVLPTLKITNSPKLISCRSEVDACATAYM 300  
; PRIOR APPLICATION NUMBER: 60/088026  
; PRIOR FILING DATE: 1998-06-04  
Qy 301 SPEELLRAWIS 311  
; PRIOR APPLICATION NUMBER: 60/088028  
; PRIOR FILING DATE: 1998-06-04  
Db 301 SPEELLRAWIS 311  
; PRIOR APPLICATION NUMBER: 60/088029  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088030  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088033  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088326  
; PRIOR FILING DATE: 1998-06-04  
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; PRIOR FILING DATE: 1998-06-16  
; PRIOR APPLICATION NUMBER: 60/089512  
; PRIOR FILING DATE: 1998-06-16  
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; PRIOR FILING DATE: 1998-06-17  
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; PRIOR FILING DATE: 1998-06-17  
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; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089599  
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; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089907  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089908  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089947  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/089948  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/089948

RESULT 2  
US-09-991-181-183  
; Sequence 183, Application US/09991181  
; Patent No. 6913919  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Klijavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC53  
; CURRENT APPLICATION NUMBER: US/09/991,181  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
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; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
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; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
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; PRIOR APPLICATION NUMBER: 60/087609  
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 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/091982  
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 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1644; DB 2; Length 311;  
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 Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 121 TSAMSLKHPPFNENSTILTRPGMEITKDGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180  
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 ; Sequence 352, Application US/09999833A  
 ; Patent No. 6916648  
 ; GENERAL INFORMATION: ---  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;  
 ; APPLICANT: Faoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumaas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630PIC65  
 ; CURRENT APPLICATION NUMBER: US/09/999,833A  
 ; CURRENT FILING DATE: 2001-10-24  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
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 ; PRIOR FILING DATE: 1997-10-17  
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 ; PRIOR APPLICATION NUMBER: 60/065311  
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 ; PRIOR FILING DATE: 1998-03-10

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; PRIOR APPLICATION NUMBER: 60/085580
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1644; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e-165;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 SPEELLRAWIS 311
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCES: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440

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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC27  
CURRENT APPLICATION NUMBER: US/09/997,333  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676

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; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090678  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090690  
; PRIOR FILING DATE: 1998-06-25  
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; PRIOR FILING DATE: 1998-06-25  
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; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090696  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090862  
; PRIOR FILING DATE: 1998-06-26  
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; PRIOR FILING DATE: 1998-07-01  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091544  
; PRIOR FILING DATE: 1998-07-01  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091626  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1644; DB 2; Length 311;

Best Local Similarity 100.0%; Pred. No. 1.8e-165;  
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTFTVLEIWTSLPMWFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSPIAP 60  
DB 1 MDTFTVLEIWTSLPMWFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSPIAP 60  
QY 61 GETVYVSVEQYESLYTSHIWPSSWCSLTGEPCEVDITATVPYNLRVATLGSQ 120  
DB 61 GETVYVSVEQYESLYTSHIWPSSWCSLTGEPCEVDITATVPYNLRVATLGSQ 120  
QY 121 TSAWSILKHPFNNSITLTPGMEITKDGPHLVIELEDLGPQEFVLVAYWRREPGEAEHV 180  
DB 121 TSAWSILKHPFNNSITLTPGMEITKDGPHLVIELEDLGPQEFVLVAYWRREPGEAEHV 180  
QY 181 KMRSGGIPVHLETMPGGAAYCVKAOTFVKATGRYSAFSQTECVEQGEAIPLVLALFAP 240  
DB 181 KMRSGGIPVHLETMPGGAAYCVKAOTFVKATGRYSAFSQTECVEQGEAIPLVLALFAP 240  
QY 241 VGFMLILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAYM 300  
DB 241 VGFMLILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAYM 300  
QY 301 SPEELLRAWIS 311  
DB 301 SPEELLRAWIS 311

RESULT 6

US-09-992-598-183  
; Sequence 183, Application US/09992598  
; Patent No. 6956108  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.

;  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087609  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087759  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087827  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: 60/088021  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088025  
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; PRIOR APPLICATION NUMBER: 60/088026  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088028  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088029  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088030  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088033  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088326  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088167  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/088202  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/088212





Db 301 SPEELRAWIS 311

RESULT 7

US-10-020-445A-352

; Sequence 352, Application US/10020445A

; Patent No. 6962797

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kijavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C74

; CURRENT APPLICATION NUMBER: US/10/020,445A

; CURRENT FILING DATE: 2001-10-24

; PRIOR APPLICATION NUMBER: 09/918595

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

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; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/078004

; PRIOR FILING DATE: 1998-03-13

; PRIOR APPLICATION NUMBER: 60/078886

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078936

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078939

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079664

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/079663

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

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; PRIOR FILING DATE: 1998-03-27

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; PRIOR FILING DATE: 1998-03-30

; PRIOR APPLICATION NUMBER: 60/079923

; PRIOR FILING DATE: 1998-03-30

; PRIOR APPLICATION NUMBER: 60/080105

; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: 60/080107

; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: 60/080165

; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: 60/080194

; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: 60/080327

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/080328

; PRIOR FILING DATE: 1998-04-01

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; PRIOR FILING DATE: 1998-04-01

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; PRIOR FILING DATE: 1998-04-27

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; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/083392

; PRIOR FILING DATE: 1998-04-29

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; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1644; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e-165;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MOTFTVNLBEIWTSLPFWFYYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLWMSVPIAP 60
DB      1  MOTFTVNLBEIWTSLPFWFYYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLWMSVPIAP 60
QY      61  GETVYYSVYQGBYESLYTSHIWPSSCSLTGPECDVTDDITATVPYNLRVRATLGSO 120
DB      61  GETVYYSVYQGBYESLYTSHIWPSSCSLTGPECDVTDDITATVPYNLRVRATLGSO 120
QY      121  TSAWSILKHPFNNSILTRPGMEITKDGPHLVIELEDLGQPEFLVAYWRREPGAEHV 180

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RESULT 8

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US-09-265-540E-2
; Sequence 2, Application US/09265540E
; Patent No. 6586228
; GENERAL INFORMATION:
; APPLICANT: Parham, Christi L.
; APPLICANT: Moore, Kevin W.
; APPLICANT: Murgolo, Nicholas J.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: HUMAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0804K
; CURRENT APPLICATION NUMBER: US/09/265,540E
; CURRENT FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 60/077,329
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (146)..(146)
; OTHER INFORMATION: The 'Xaa' at location 146 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (148)..(148)
; OTHER INFORMATION: The 'Xaa' at location 148 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (171)..(171)
; OTHER INFORMATION: The 'Xaa' at location 171 stands for Arg, or Thr.
; NAME/KEY: misc feature
; LOCATION: (214)..(214)
; OTHER INFORMATION: The 'Xaa' at location 214 stands for Arg, or Lys.
; NAME/KEY: misc feature
; LOCATION: (567)..(567)
; OTHER INFORMATION: unknown nucleotide
; NAME/KEY: misc feature
; LOCATION: (573)..(573)
; OTHER INFORMATION: unknown nucleotide
; NAME/KEY: misc feature
; LOCATION: (1336)..(1336)
; OTHER INFORMATION: unknown nucleotide
; NAME/KEY: misc feature
; LOCATION: (1369)..(1369)
; OTHER INFORMATION: unknown nucleotide
US-09-265-540E-2

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Query Match 98.5%; Score 1620; DB 2; Length 311;  
Best Local Similarity 98.7%; Pred. No. 6.3e-163;  
Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MOTFTVNLBEIWTSLPFWFYYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLWMSVPIAP 60

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Db      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
QY      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDDITATVPYNLRVRATLGSQ 120
Db      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDDITATVPYNLRVRATLGSQ 120
QY      121  TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180
Db      121  TSAWSILKHPFNRRNSTILTRPGMEIKXGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180
QY      181  KMYRSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240
Db      181  KMYRSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240
QY      241  VGFMILLVVVPLFVWKMGRLLOYSQCPVVVLPDTLKITNSPQKLSICRREEVDACATVM 300
Db      241  VGFMILLVVVPLFVWKMGRLLOYSQCPVVVLPDTLKITNSPQKLSICRREEVDACATVM 300
QY      301  SPEELRAWIS 311
Db      301  SPEELRAWIS 311

RESULT 9
US-09-746-359A-19
; Sequence 19, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-19

Query Match      89.8%; Score 1477; DB 2; Length 301;
Best Local Similarity 98.9%; Pred. No. 8.2e-148;
Matches 279; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
Db      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
QY      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDDITATVPYNLRVRATLGSQ 120
Db      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDDITATVPYNLRVRATLGSQ 120
QY      121  TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180
Db      121  TSAWSILKHPFNRRNSTILTRPGMEIPKHGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180
QY      181  KMYRSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240
Db      181  KMYRSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240
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Db      181  KMYRSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240
QY      241  VGFMILLVVVPLFVWKMGRLLOYSQCPVVVLPDTLKITNSPQ 282
Db      241  VGFMILLVVVPLFVWKMGRLLOYSQCPVVVLPDTLKITNSPQ 282

RESULT 10
US-09-746-359A-57
; Sequence 57, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-57

Query Match      75.1%; Score 1234.5; DB 2; Length 336;
Best Local Similarity 85.9%; Pred. No. 4.6e-122;
Matches 238; Conservative 7; Mismatches 17; Indels 15; Gaps 2;

QY      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
Db      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
QY      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDDITATVPYNLRVRATLGSQ 120
Db      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDDITATVPYNLRVRATLGSQ 120
QY      121  TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180
Db      121  TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180
QY      181  KMYRSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240
Db      181  KMYRSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240
QY      241  -----VGFMILLVVVPLFV-----WKMGRLQ 262
Db      241  PPSDEQLKSGTASVVCCLANNFYPREAKVQMKVDNALQ 277

RESULT 11
US-10-233-873A-2
; Sequence 2, Application US/10233873A
; Patent No. 6902930
; GENERAL INFORMATION:
; APPLICANT: Peng Liang
; TITLE OF INVENTION: THE HUMAN MOB-5 (IL-24) RECEPTORS AND USES THEREOF
; FILE REFERENCE: 22000.0091U4
; CURRENT APPLICATION NUMBER: US/10/233,873A
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; CURRENT FILING DATE: 2002-11-29  
; PRIOR APPLICATION NUMBER: 60/315,684  
; PRIOR FILING DATE: 2001-08-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; No. 6902930e =  
; OTHER INFORMATION: Synthetic Construct  
US-10-233-873A-2

Query Match 74.1%; Score 1218; DB 2; Length 229;  
Best Local Similarity 99.8%; Pred. No. 1.4e-120; Indels 0; Gaps 0;  
Matches 228; Conservative 0; Mismatches 1;  
Db 1 MOTFTVBLEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSVPIAP 60  
Db 1 MOTFTVBLEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSVPIAP 60  
Qy 61 GETVYVSVEYQGEYSLYTSHTWIPSSWCSLSTEGPCDVTDDITATVPYNLRVATLGSQ 120  
Db 61 GETVYVSVEYQGEYSLYTSHTWIPSSWCSLSTEGPCDVTDDITATVPYNLRVATLGSQ 120  
Qy 121 TSWSILKHPFNRSNLTIRPGMEITKDGFLHVLIELEDLGPQEFVLVAYWRREPGEAEHV 180  
Db 121 TSWSILKHPFNRSNLTIRPGMEITKDGFLHVLIELEDLGPQEFVLVAYWRREPGEAEHV 180  
Qy 181 KMRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECEVQGE 229  
Db 181 KMRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECEVQGE 229

RESULT 12  
US-09-746-359A-21  
; Sequence 21, Application US/09746359A  
; Patent No. 6610286  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Eagan, Maribeth A.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Chandrasekhar, Yasmin A.  
; APPLICANT: No. 6610286ak, Julia E.  
; FILE REFERENCE: 99-108  
; TITLE OF INVENTION: Method for Treating Inflammation  
; CURRENT APPLICATION NUMBER: US/09/746,359A  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-746-359A-21

Query Match 73.5%; Score 1209; DB 2; Length 352;  
Best Local Similarity 98.7%; Pred. No. 2.5e-119;  
Matches 227; Conservative 0; Mismatches 1;  
Indels 0; Gaps 0;  
Qy 1 MOTFTVBLEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSVPIAP 60

Db 1 MOTFTVBLEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSVPIAP 60  
Qy 61 GETVYVSVEYQGEYSLYTSHTWIPSSWCSLSTEGPCDVTDDITATVPYNLRVATLGSQ 120  
Db 61 GETVYVSVEYQGEYSLYTSHTWIPSSWCSLSTEGPCDVTDDITATVPYNLRVATLGSQ 120  
Qy 121 TSWSILKHPFNRSNLTIRPGMEITKDGFLHVLIELEDLGPQEFVLVAYWRREPGEAEHV 180  
Db 121 TSWSILKHPFNRSNLTIRPGMEITKDGFLHVLIELEDLGPQEFVLVAYWRREPGEAEHV 180  
Qy 181 KMRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECEVQGE 230  
Db 181 KMRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECEVQGE 230

RESULT 13  
US-09-746-359A-15  
; Sequence 15, Application US/09746359A  
; Patent No. 6610286  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Eagan, Maribeth A.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Chandrasekhar, Yasmin A.  
; APPLICANT: No. 6610286ak, Julia E.  
; TITLE OF INVENTION: Method for Treating Inflammation  
; FILE REFERENCE: 99-108  
; CURRENT APPLICATION NUMBER: US/09/746,359A  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-746-359A-15

Query Match 65.7%; Score 1080; DB 2; Length 203;  
Best Local Similarity 100.0%; Pred. No. 4.9e-106;  
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 30 DEVAIPAPQNLVSLTNMKHLLMWSVPIAPGETVYVSVEYQGEYSLYTSHTWIPSSWC 89  
Db 1 DEVAIPAPQNLVSLTNMKHLLMWSVPIAPGETVYVSVEYQGEYSLYTSHTWIPSSWC 60  
Qy 90 SLTEGPCDVTDDITATVPYNLRVATLGSQTSAMSILKHPFNRSNLTIRPGMEITKDG 149  
Db 61 SLTEGPCDVTDDITATVPYNLRVATLGSQTSAMSILKHPFNRSNLTIRPGMEITKDG 120  
Qy 150 FHLVIELEDLGPQEFVLVAYWRREPGEAEHVXKMRSGGIPVHLETMEPGAAYCVKAQTFV 209  
Db 121 FHLVIELEDLGPQEFVLVAYWRREPGEAEHVXKMRSGGIPVHLETMEPGAAYCVKAQTFV 180  
Qy 210 KAIGRYSAFSGTECEVQGEAIP 232  
Db 181 KAIGRYSAFSGTECEVQGEAIP 203

RESULT 14  
US-09-746-359A-58  
; Sequence 58, Application US/09746359A  
; Patent No. 6610286  
; GENERAL INFORMATION:

; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Eagan, Maribeth A.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Chandrasekher, Yasmin A.  
; APPLICANT: No. 6610286ak, Julia E.  
; TITLE OF INVENTION: Method for Treating Inflammation  
; FILE REFERENCE: 99-108  
; CURRENT APPLICATION NUMBER: US/09/746,359A  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 58  
; LENGTH: 307  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-746-359A-58

Query Match 65.4%; Score 1075.5; DB 2; Length 307;  
Best Local Similarity 84.3%; Pred. No. 2.7e-105;  
Matches 209; Conservative 7; Mismatches 17; Indels 15; Gaps 2;  
  
QY 30 DEVAIIAPQNLVSLSTNMKHLIMWSPVIAPGETVYYSVEYQGEYESLYTSHIWPSSWC 89  
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Db 1 DEVAIIAPQNLVSLSTNMKHLIMWSPVIAPGETVYYSVEYQGEYESLYTSHIWPSSWC 60  
|||  
  
QY 90 SLTEGPECDDTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG 149  
|||  
Db 61 SLTEGPECDDTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG 120  
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QY 150 FHLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSGGIPVHLETMEPGAAAYCVKAQTFV 209  
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Db 121 FHLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSGGIPVHLETMEPGAAAYCVKAQTFV 180  
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QY 210 KAIGRYSAFSQTECVQGEATPLVLAFAF-----VGFMLILVVVPLFV----- 254  
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Db 181 KAIGRYSAFSQTECVQGEATVAAPSVFIFFPPSDQLKSGTASVVCLLNFFYPREAKVQ 240  
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QY 255 WKMGRLQ 262  
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Db 241 WKVDNALQ 248  
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RESULT 15  
US-09-746-359A-59  
; Sequence 59, Application US/09746359A  
; Patent No. 6610286  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Eagan, Maribeth A.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Chandrasekher, Yasmin A.  
; APPLICANT: No. 6610286ak, Julia E.  
; TITLE OF INVENTION: Method for Treating Inflammation  
; FILE REFERENCE: 99-108  
; CURRENT APPLICATION NUMBER: US/09/746,359A  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969

; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 59  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-746-359A-59  
  
Query Match 65.0%; Score 1069; DB 2; Length 201;  
Best Local Similarity 100.0%; Pred. No. 7e-105;  
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 30 DEVAIIAPQNLVSLSTNMKHLIMWSPVIAPGETVYYSVEYQGEYESLYTSHIWPSSWC 89  
|||  
Db 1 DEVAIIAPQNLVSLSTNMKHLIMWSPVIAPGETVYYSVEYQGEYESLYTSHIWPSSWC 60  
|||  
  
QY 90 SLTEGPECDDTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG 149  
|||  
Db 61 SLTEGPECDDTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG 120  
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QY 150 FHLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSGGIPVHLETMEPGAAAYCVKAQTFV 209  
|||  
Db 121 FHLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSGGIPVHLETMEPGAAAYCVKAQTFV 180  
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QY 210 KAIGRYSAFSQTECVQGEA 230  
|||  
Db 181 KAIGRYSAFSQTECVQGEA 201  
|||  
  
Search completed: April 5, 2006, 11:42:59  
Job time : 25.1169 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:41:13 ; Search time 42.8831 Seconds  
(without alignments)  
1066.146 Million cell updates/sec

Title: US-09-745-792A-11

Perfect score: 2947

Sequence: 1 MRAPGRPALRPPLPPLLLL.....NETYLMQFMENGLYQVQEN 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/ptodata/1/iaa/6-COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2947	100.0	553	1	US-08-943-087-2 ✓
2	2947	100.0	553	1	US-08-943-087-14
3	2947	100.0	553	1	US-08-943-087-16
4	2947	100.0	553	1	US-08-943-087-18
5	2947	100.0	553	1	US-08-943-087-20
6	2947	100.0	553	1	US-08-943-087-22
7	2947	100.0	553	1	US-08-943-087-24
8	2947	100.0	553	1	US-08-943-087-26
9	2947	100.0	553	1	US-08-943-087-28
10	2947	100.0	553	1	US-08-943-087-30
11	2947	100.0	553	1	US-08-943-087-32
12	2947	100.0	553	1	US-08-943-087-34
13	2947	100.0	553	1	US-08-943-087-36
14	2947	100.0	553	1	US-08-943-087-38
15	2947	100.0	553	1	US-08-943-087-40
16	2947	100.0	553	1	US-08-943-087-42
17	2947	100.0	553	1	US-08-943-087-44
18	2947	100.0	553	1	US-08-943-087-46
19	2947	100.0	553	1	US-08-943-087-48
20	2947	100.0	553	2	US-09-746-359A-11 ✓
21	2947	100.0	553	2	US-09-861-779-2
22	2947	100.0	553	2	US-09-949-016-6873
23	2947	100.0	553	2	US-10-233-873A-7
24	2941	99.8	567	2	US-09-949-016-11502
25	2203	74.8	442	2	US-10-012-231A-104
26	2203	74.8	442	2	US-10-015-389A-104
27	2203	74.8	442	2	US-10-006-768A-104

28	2203	74.8	442	2	US-10-015-671A-104	Sequence 104, App
29	2203	74.8	442	2	US-10-015-393A-104	Sequence 104, App
30	2203	74.8	442	2	US-10-011-833A-104	Sequence 104, App
31	2203	74.8	442	2	US-10-006-041A-104	Sequence 104, App
32	2203	74.8	442	2	US-10-012-064A-104	Sequence 104, App
33	1769.5	60.0	546	2	US-09-746-359A-37	Sequence 37, Appl
34	1715	58.2	514	2	US-09-746-359A-39	Sequence 39, Appl
35	1344	45.6	248	2	US-10-233-873A-3	Sequence 3, Appl1
36	1294.5	43.9	571	2	US-09-746-359A-53	Sequence 53, Appl
37	1200	40.7	221	1	US-08-943-087-50	Sequence 50, Appl
38	1200	40.7	221	1	US-09-746-359A-12	Sequence 12, Appl
39	1196	40.6	221	1	US-08-943-087-54	Sequence 54, Appl
40	1192	40.4	221	1	US-08-943-087-52	Sequence 52, Appl
41	1184	40.2	221	1	US-08-943-087-56	Sequence 56, Appl
42	1183	40.1	547	2	US-09-746-359A-54	Sequence 54, Appl
43	1182	40.1	221	1	US-08-943-087-58	Sequence 58, Appl
44	1180	40.0	217	2	US-09-746-359A-55	Sequence 55, Appl
45	1171	39.7	594	2	US-09-746-359A-23	Sequence 23, Appl

## ALIGNMENTS

## RESULT 1

US-08-943-087-2  
; Sequence 2, Application US/08943087  
; Patent No. 5945511  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-943-087-2

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Query Match      100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINKNVLOWTPPE 60
Db 1 MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINKNVLOWTPPE 60
QY 61 GLOGVKVTVTVQYFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIMGTKC 120
Db 61 GLOGVKVTVTVQYFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIMGTKC 120
QY 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPKWKNPEDLPVSMQIYSNLK 180
Db 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPKWKNPEDLPVSMQIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDFKRF 300
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDFKRF 300
QY 301 FVPAEKIVINFITLNISSDSDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360
Db 301 FVPAEKIVINFITLNISSDSDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVEIYEDVVRTTIDICAGPEQEELS 420
Db 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVEIYEDVVRTTIDICAGPEQEELS 420
QY 421 LQEEVSTQGTLLSQAAALVGLPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
Db 421 LQEEVSTQGTLLSQAAALVGLPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
QY 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEAPADPRPPGENETYLMQ 540
Db 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEAPADPRPPGENETYLMQ 540
QY 541 FMEEWGLYQOMEN 553
Db 541 FMEEWGLYQOMEN 553

RESULT 3
US-08-943-087-14
; Sequence 14, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:

; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-943-087-14

Query Match      100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINKNVLOWTPPE 60
Db 1 MRAPGRPALRPLPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINKNVLOWTPPE 60
QY 61 GLOGVKVTVTVQYFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIMGTKC 120
Db 61 GLOGVKVTVTVQYFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIMGTKC 120
QY 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPKWKNPEDLPVSMQIYSNLK 180
Db 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPKWKNPEDLPVSMQIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDFKRF 300
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDFKRF 300
QY 301 FVPAEKIVINFITLNISSDSDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360
Db 301 FVPAEKIVINFITLNISSDSDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVEIYEDVVRTTIDICAGPEQEELS 420
Db 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVEIYEDVVRTTIDICAGPEQEELS 420
QY 421 LQEEVSTQGTLLSQAAALVGLPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
Db 421 LQEEVSTQGTLLSQAAALVGLPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
QY 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEAPADPRPPGENETYLMQ 540
Db 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEAPADPRPPGENETYLMQ 540
QY 541 FMEEWGLYQOMEN 553
Db 541 FMEEWGLYQOMEN 553

RESULT 3
US-08-943-087-16
; Sequence 16, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
```





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QY 61 GLQGVKVTYTVQYFYIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTC 120
|
|
|
Db 61 GLQGVKVTYTVQYFYIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTC 120
|
|
|
QY 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
|
|
|
Db 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
|
|
|
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRAQPKOCARTL 240
|
|
|
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRAQPKOCARTL 240
|
|
|
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYIGNEFDKRF 300
|
|
|
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYIGNEFDKRF 300
|
|
|
QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQSGNLRLPPOEEBEVKHL 360
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|
|
Db 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQSGNLRLPPOEEBEVKHL 360
|
|
|
QY 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVVTRTTDICAGPEQELS 420
|
|
|
Db 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVVTRTTDICAGPEQELS 420
|
|
|
QY 421 LOEEVSTQGTLLSQAAALAVLGPQTLOYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
|
|
|
Db 421 LOEEVSTQGTLLSQAAALAVLGPQTLOYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
|
|
|
QY 481 DNDPQTRGLCIPSLSSFDQSGCEPSEGDGLGEEGLLSRLYEAPADPPGNETYLMQ 540
|
|
|
Db 481 DNDPQTRGLCIPSLSSFDQSGCEPSEGDGLGEEGLLSRLYEAPADPPGNETYLMQ 540
|
|
|
QY 541 FMEEWGLYVQMEN 553
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|
|
Db 541 FMEEWGLYVQMEN 553
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|
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## RESULT 5

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US-08-943-087-20
; Sequence 20, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
```

```
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLSCULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-20

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60
|
|
|
Db 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60
|
|
|
QY 61 GLQGVKVTYTVQYFYIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTC 120
|
|
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Db 61 GLQGVKVTYTVQYFYIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTC 120
|
|
|
QY 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
|
|
|
Db 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
|
|
|
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRAQPKOCARTL 240
|
|
|
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRAQPKOCARTL 240
|
|
|
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYIGNEFDKRF 300
|
|
|
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYIGNEFDKRF 300
|
|
|
QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQSGNLRLPPOEEBEVKHL 360
|
|
|
Db 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQSGNLRLPPOEEBEVKHL 360
|
|
|
QY 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVVTRTTDICAGPEQELS 420
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|
|
Db 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVVTRTTDICAGPEQELS 420
|
|
|
QY 421 LOEEVSTQGTLLSQAAALAVLGPQTLOYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
|
|
|
Db 421 LOEEVSTQGTLLSQAAALAVLGPQTLOYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
|
|
|
QY 481 DNDPQTRGLCIPSLSSFDQSGCEPSEGDGLGEEGLLSRLYEAPADPPGNETYLMQ 540
|
|
|
Db 481 DNDPQTRGLCIPSLSSFDQSGCEPSEGDGLGEEGLLSRLYEAPADPPGNETYLMQ 540
|
|
|
QY 541 FMEEWGLYVQMEN 553
|
|
|
Db 541 FMEEWGLYVQMEN 553
|
|
|

RESULT 6
US-08-943-087-22
; Sequence 22, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
```

```
/
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ZymoGenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,087
/ FILING DATE:
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/803,305
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-08-943-087-22

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
Db 1 MRAPGRPALRLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
QY 61 GLQGVKVTYTVQYFYIYQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
Db 61 GLQGVKVTYTVQYFYIYQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
QY 121 SKWASGRPYPLETQIGPPEVALTTDEKSI SVLTAPKWKRNRPDLPVSMQOIYSNLK 180
Db 121 SKWASGRPYPLETQIGPPEVALTTDEKSI SVLTAPKWKRNRPDLPVSMQOIYSNLK 180
QY 181 YNVSVLNTKSNRTWSCVNTHTLVLTWLPNTLYCVHVESFVPGPPRAQPKQKARTL 240
Db 181 YNVSVLNTKSNRTWSCVNTHTLVLTWLPNTLYCVHVESFVPGPPRAQPKQKARTL 240
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNFDPKRF 300
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNFDPKRF 300
QY 301 FVPAEKIVNFTLNTSDSKISHQMSLLGKSSDVSSINDPQPSGNLRPPQEEERVKHL 360
Db 301 FVPAEKIVNFTLNTSDSKISHQMSLLGKSSDVSSINDPQPSGNLRPPQEEERVKHL 360
QY 361 GYASHLMIEFCDSEENTEGTSFTQBSLSRTIPPKDTVIEYDVVTTDTCAGPEOELS 420
Db 361 GYASHLMIEFCDSEENTEGTSFTQBSLSRTIPPKDTVIEYDVVTTDTCAGPEOELS 420
QY 421 LOBEVSTQGTLLSQAALAVLGPQTQYSVTPQLQDLPLAQBHTDSERGPPEPSTTLV 480
Db 421 LOBEVSTQGTLLSQAALAVLGPQTQYSVTPQLQDLPLAQBHTDSERGPPEPSTTLV 480

CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-22

CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-24

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
Db 1 MRAPGRPALRLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINNKNVLTWTPPE 60
QY 61 GLQGVKVTYTVQYFYIYQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
Db 61 GLQGVKVTYTVQYFYIYQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
QY 121 SKWASGRPYPLETQIGPPEVALTTDEKSI SVLTAPKWKRNRPDLPVSMQOIYSNLK 180
Db 121 SKWASGRPYPLETQIGPPEVALTTDEKSI SVLTAPKWKRNRPDLPVSMQOIYSNLK 180
```

Db 121 SKWASGRYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKRNPEDLPVSMQOIYSNLK 180  
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240  
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240  
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILIIYGNEDFKRF 300  
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILIIYGNEDFKRF 300  
QY 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSDVSSLNDPQSGNLPRPQSEEVVKHL 360  
Db 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSDVSSLNDPQSGNLPRPQSEEVVKHL 360  
QY 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVEIYEYDVRTTIDICAGPEQELS 420  
Db 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVEIYEYDVRTTIDICAGPEQELS 420  
QY 421 LQEEVSTQGLLESQAALAVLGPQTLYSYTTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480  
Db 421 LQEEVSTQGLLESQAALAVLGPQTLYSYTTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480  
QY 481 DWDPTQRLCIPSLSSFDQDSEGCPSSEGDGLGEEGLSRLYEPAEDRPPGNETYLMQ 540  
Db 481 DWDPTQRLCIPSLSSFDQDSEGCPSSEGDGLGEEGLSRLYEPAEDRPPGNETYLMQ 540  
QY 541 FMEEWGLYVQMEN 553  
Db 541 FMEEWGLYVQMEN 553

RESULT 8

US-08-943-087-26  
; Sequence 26, Application US/08943087  
; Patent No. 5945511  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmeberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
;

; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-943-087-26  
  
Query Match 100.0%; Score 2947; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 1.6e-267;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRAPGRPALRPPLPPLLLLAAPWGRAVPCVSGGLPKPANITFLISINMKVLTWTPPE 60  
Db 1 MRAPGRPALRPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLISINMKVLTWTPPE 60  
QY 61 GLQGVKVTYVQYFIYGQKKWLKSECRNINITYCDLSAETSDYEHQYAKVKAIWGTKC 120  
Db 61 GLQGVKVTYVQYFIYGQKKWLKSECRNINITYCDLSAETSDYEHQYAKVKAIWGTKC 120  
QY 121 SKWASGREYFPLETOIGPPEVALTTDEKSI SVLTAPEKWKRNPEDLPVSMQOIYSNLK 180  
Db 121 SKWASGREYFPLETOIGPPEVALTTDEKSI SVLTAPEKWKRNPEDLPVSMQOIYSNLK 180  
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240  
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240  
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILIIYGNEDFKRF 300  
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILIIYGNEDFKRF 300  
QY 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSDVSSLNDPQSGNLPRPQSEEVVKHL 360  
Db 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSDVSSLNDPQSGNLPRPQSEEVVKHL 360  
QY 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVEIYEYDVRTTIDICAGPEQELS 420  
Db 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVEIYEYDVRTTIDICAGPEQELS 420  
QY 421 LQEEVSTQGLLESQAALAVLGPQTLYSYTTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480  
Db 421 LQEEVSTQGLLESQAALAVLGPQTLYSYTTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480  
QY 481 DWDPTQRLCIPSLSSFDQDSEGCPSSEGDGLGEEGLSRLYEPAEDRPPGNETYLMQ 540  
Db 481 DWDPTQRLCIPSLSSFDQDSEGCPSSEGDGLGEEGLSRLYEPAEDRPPGNETYLMQ 540  
QY 541 FMEEWGLYVQMEN 553  
Db 541 FMEEWGLYVQMEN 553

RESULT 9

US-08-943-087-28  
; Sequence 28, Application US/08943087  
; Patent No. 5945511  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmeberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
;

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-28

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
DB 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
QY 61 GLOGKVTVTVQVFIYQKKWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
DB 61 GLOGKVTVTVQVFIYQKKWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
QY 121 SKWASGRYPFPLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPEDLPVSMQOIYSNLK 180
DB 121 SKWASGRYPFPLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPEDLPVSMQOIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
DB 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
QY 241 KQOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNFDFKRF 300
DB 241 KQOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNFDFKRF 300
QY 301 FVPAEKIVNFTLNISDDSKISHQDMSLLGKSSDVSLNDPOPSGNLRPPQPEEEVKHL 360
DB 301 FVPAEKIVNFTLNISDDSKISHQDMSLLGKSSDVSLNDPOPSGNLRPPQPEEEVKHL 360
QY 361 GYASHLMEIFCDSEENETGTSFTQOSLSRTIIPDKTVIEYVDVTTDTCAGPEEQELS 420
DB 361 GYASHLMEIFCDSEENETGTSFTQOSLSRTIIPDKTVIEYVDVTTDTCAGPEEQELS 420
QY 421 LQEVSTQGTLLBSQAALAVLGQTTLQYSYTPQLDLDPLAQSHDTSEEGPEEPSTTLV 480
DB 421 LQEVSTQGTLLBSQAALAVLGQTTLQYSYTPQLDLDPLAQSHDTSEEGPEEPSTTLV 480
QY 481 DWDPTQGRICPSLSFDQSEGCPSSEGGGLGEEGLLSRLYEEDPADPPPGNETYILMQ 540
DB 481 DWDPTQGRICPSLSFDQSEGCPSSEGGGLGEEGLLSRLYEEDPADPPPGNETYILMQ 540
QY 541 FMEEWGLYVQMEN 553
DB 541 FMEEWGLYVQMEN 553
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```

RESULT 10
US-08-943-087-30
; Sequence 30, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-30

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
DB 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
QY 61 GLOGKVTVTVQVFIYQKKWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
DB 61 GLOGKVTVTVQVFIYQKKWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
QY 121 SKWASGRYPFPLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPEDLPVSMQOIYSNLK 180
DB 121 SKWASGRYPFPLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPEDLPVSMQOIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
DB 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
QY 241 KQOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNFDFKRF 300
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Db 241 KDOSSEFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILLYGNEFDKRF 300  
Qy 301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL 360  
Db 301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL 360  
Qy 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTTIPDKTVIEYEDVVRTTIDICAGPEQELS 420  
Db 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTTIPDKTVIEYEDVVRTTIDICAGPEQELS 420  
Qy 421 LQEEVSTQGTLLSQAALAVLPQTLYSYTTQLOQLDPLAQEHTDSESGPEEPSTTLV 480  
Db 421 LQEEVSTQGTLLSQAALAVLPQTLYSYTTQLOQLDPLAQEHTDSESGPEEPSTTLV 480  
Qy 481 DWDPTQGRLCIPSLSFDDQSGCEPSEGDGLGEGLLSRLYEAPDRPPGENETYLMQ 540  
Db 481 DWDPTQGRLCIPSLSFDDQSGCEPSEGDGLGEGLLSRLYEAPDRPPGENETYLMQ 540  
Qy 541 FMEEWGLYVQMEN 553  
Db 541 FMEEWGLYVQMEN 553

RESULT 11  
US-08-943-087-32  
; Sequence 32, Application US/08943087  
; Patent No. 5945511  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-943-087-32

Query Match 100.0%; Score 2947; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 1.6e-267;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60  
Db 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60  
Qy 61 GLOGVKVTVTVQYFIYGOKKWLKSECRNINITYCDLSAETSDYEHQYAKVKAIWGTC 120  
Db 61 GLOGVKVTVTVQYFIYGOKKWLKSECRNINITYCDLSAETSDYEHQYAKVKAIWGTC 120  
Qy 121 SKWASRGREYFLETOIGPPEVALTTDEKSI SVLTAPKWKRNRPDLFVSMQOIYSNLK 180  
Db 121 SKWASRGREYFLETOIGPPEVALTTDEKSI SVLTAPKWKRNRPDLFVSMQOIYSNLK 180  
Qy 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240  
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240  
Qy 241 KDOSSEFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILLYGNEFDKRF 300  
Db 241 KDOSSEFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILLYGNEFDKRF 300  
Qy 301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL 360  
Db 301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL 360  
Qy 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTTIPDKTVIEYEDVVRTTIDICAGPEQELS 420  
Db 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTTIPDKTVIEYEDVVRTTIDICAGPEQELS 420  
Qy 421 LQEEVSTQGTLLSQAALAVLPQTLYSYTTQLOQLDPLAQEHTDSESGPEEPSTTLV 480  
Db 421 LQEEVSTQGTLLSQAALAVLPQTLYSYTTQLOQLDPLAQEHTDSESGPEEPSTTLV 480  
Qy 481 DWDPTQGRLCIPSLSFDDQSGCEPSEGDGLGEGLLSRLYEAPDRPPGENETYLMQ 540  
Db 481 DWDPTQGRLCIPSLSFDDQSGCEPSEGDGLGEGLLSRLYEAPDRPPGENETYLMQ 540  
Qy 541 FMEEWGLYVQMEN 553  
Db 541 FMEEWGLYVQMEN 553

RESULT 12  
US-08-943-087-34  
; Sequence 34, Application US/08943087  
; Patent No. 5945511  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087

FILING DATE: 536  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA: 08/803,305  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-943-087-34

Query Match 100.0%; Score 2947; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 1.6e-267;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPLPPLLLLLLAAWGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
DB 1 MRAPGRPALRPLPLPPLLLLLLAAWGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
QY 61 GLOGVKVTVTVQVFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120  
DB 61 GLOGVKVTVTVQVFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120  
QY 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPKWKKNRPEDLPVSMQOIYSNLK 180  
DB 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPKWKKNRPEDLPVSMQOIYSNLK 180  
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVSVFVPGPPRRAPQSEKQCARTL 240  
DB 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVSVFVPGPPRRAPQSEKQCARTL 240  
QY 241 KOQSEFEKAKIIFWVLPISITVFLPSVMGYSIYRIVHVGKEKHPANLILYGNFEDKRF 300  
DB 241 KOQSEFEKAKIIFWVLPISITVFLPSVMGYSIYRIVHVGKEKHPANLILYGNFEDKRF 300  
QY 301 FVPAEKIVINFITLNI SDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEEVKHL 360  
DB 301 FVPAEKIVINFITLNI SDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEEVKHL 360

RESULT 13  
US-08-943-087-36  
Sequence 36, Application US/08943087  
Patent No. 5945511  
GENERAL INFORMATION:

APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmsberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore B.  
APPLICANT: Farrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-943-087-36

Query Match 100.0%; Score 2947; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 1.6e-267;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPLPPLLLLLLAAWGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
DB 1 MRAPGRPALRPLPLPPLLLLLLAAWGRAVPCVSGGLPKPANITFLSINKNVLTWTPPE 60  
QY 61 GLOGVKVTVTVQVFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120  
DB 61 GLOGVKVTVTVQVFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120  
QY 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPKWKKNRPEDLPVSMQOIYSNLK 180  
DB 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPKWKKNRPEDLPVSMQOIYSNLK 180  
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVSVFVPGPPRRAPQSEKQCARTL 240  
DB 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVSVFVPGPPRRAPQSEKQCARTL 240  
QY 241 KOQSEFEKAKIIFWVLPISITVFLPSVMGYSIYRIVHVGKEKHPANLILYGNFEDKRF 300  
DB 241 KOQSEFEKAKIIFWVLPISITVFLPSVMGYSIYRIVHVGKEKHPANLILYGNFEDKRF 300  
QY 301 FVPAEKIVINFITLNI SDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEEVKHL 360  
DB 301 FVPAEKIVINFITLNI SDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEEVKHL 360





```
;
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-943-087-40

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPLPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKVNLQWTPPE 60
Db 1 MRAPGRPALRPLPLPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKVNLQWTPPE 60
QY 61 GLOGVKVTVTVQYFIYGOKWLNKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTKC 120
Db 61 GLOGVKVTVTVQYFIYGOKWLNKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTKC 120
QY 121 SKWAESGRFPFLETOIGPPEVALTTDEKISIVLTAPEKWKKNPEDLPVSMQOIYSNLK 180
Db 121 SKWAESGRFPFLETOIGPPEVALTTDEKISIVLTAPEKWKKNPEDLPVSMQOIYSNLK 180
QY 181 YNVSVLNTRKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
Db 181 YNVSVLNTRKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
QY 241 KDQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNFEDKRF 300
Db 241 KDQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNFEDKRF 300
QY 301 FVPAEKIVINFITLINISDDSKI SHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEEVXHL 360
Db 301 FVPAEKIVINFITLINISDDSKI SHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEEVXHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQGSLSRTIPDKTVIEYDYVRTTICAGPBEQELS 420
Db 361 GYASHLMEIFCDSEENTEGTSFTQGSLSRTIPDKTVIEYDYVRTTICAGPBEQELS 420
QY 421 LOEVSTQGTLLSQAALAVLGPTQLOYSTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
Db 421 LOEVSTQGTLLSQAALAVLGPTQLOYSTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
QY 481 DWDPTQGLRCIPSLSSFDQSECEPSEGGGLGEGLLSRLYEPPADPPGNETYLMQ 540
Db 481 DWDPTQGLRCIPSLSSFDQSECEPSEGGGLGEGLLSRLYEPPADPPGNETYLMQ 540
QY 541 FMEEWGLYQVMEN 553
Db 541 FMEEWGLYQVMEN 553
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Search completed: April 5, 2006, 11:43:00  
Job time : 43.8831 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: April 5, 2006, 11:29:48 ; Search time 117.705 Seconds

(without alignments)  
1160.927 Million cell updates/sec

Title: US-09-745-792A-14

Perfect score: 1644

Sequence: 1 MQTFWVLSEIWTSLFWFF.....VDACATVMSPELLRAWIS 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Genesecp1980s:\*  
2: Genesecp1990s:\*  
3: Genesecp2000s:\*  
4: Genesecp2001s:\*  
5: Genesecp2002s:\*  
6: Genesecp2003as:\*  
7: Genesecp2003bs:\*  
8: Genesecp2004s:\*  
9: Genesecp2005s:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1644	100.0	311	2	AA41736 Human PRO
2	1644	100.0	311	3	AA46676 Membrane-
3	1644	100.0	311	3	AA33440 Human PRO
4	1644	100.0	311	3	AA44664 Interfero
5	1644	100.0	311	3	AA44292 Human PRO
6	1644	100.0	311	3	AA47046 Human TAN
7	1644	100.0	311	4	AA12187 Human PRO
8	1644	100.0	311	4	AA85270 Human IL-
9	1644	100.0	311	4	AA00339 Human cyt
10	1644	100.0	311	4	AA04059 Human int
11	1644	100.0	311	4	AA65199 Human PRO
12	1644	100.0	311	5	ABG7201 Human int
13	1644	100.0	311	5	AB90182 Human pol
14	1644	100.0	311	5	AAE23355 Human int
15	1644	100.0	311	5	AB84877 Human PRO
16	1644	100.0	311	5	AAE29064 Human IL-
17	1644	100.0	311	5	AB95483 Human ang
18	1644	100.0	311	6	AB58014 Human PRO
19	1644	100.0	311	6	ABU59092 Novel hum
20	1644	100.0	311	6	ABU82604 Human sec
21	1644	100.0	311	6	ABO17631 Novel hum
22	1644	100.0	311	6	ABU60523 Human sec
23	1644	100.0	311	6	ABO25238 Novel hum
24	1644	100.0	311	6	ABU13905 Human PRO

## ALIGNMENTS

### RESULT 1

AA41736

ID AA41736 standard; protein; 311 AA.

XX AA41736;

DT 07-DEC-1999 (first entry)

XX Human PRO1114 protein sequence.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein.

XX Homo sapiens.

XX WO9946281-A2.

PD 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 12-MAR-1998; 98US-0077649P.

PR 13-MAR-1998; 98US-0077791P.

PR 17-MAR-1998; 98US-0078004P.

PR 20-MAR-1998; 98US-0004020.

PR 20-MAR-1998; 98US-0078866P.

PR 20-MAR-1998; 98US-0078910P.

PR 20-MAR-1998; 98US-0078936P.

PR 25-MAR-1998; 98US-0078939P.

PR 26-MAR-1998; 98US-0079294P.

PR 27-MAR-1998; 98US-0079663P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079689P.

PR 27-MAR-1998; 98US-0079728P.

PR 27-MAR-1998; 98US-0079786P.

PR 30-MAR-1998; 98US-0079920P.

PR 31-MAR-1998; 98US-0079923P.

PR 31-MAR-1998; 98US-0080105P.

PR 31-MAR-1998; 98US-0080107P.

PR 31-MAR-1998; 98US-0080165P.

PR 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

PR

PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 07-MAY-1998; 98US-0084441P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086114P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.  
PR (GETH ) GENENTECH INC.  
XX  
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
XX  
XX WPI; 1999-551358/46.  
DR N-PSDB; AA234190.  
XX  
XX New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular

PT adhesion disorders.  
XX  
XX Claim 12; Fig 142; 530pp; English.  
XX  
CC The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AA233891 to AA23438, and AA41685 to  
CC AA41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention  
XX  
XX Sequence 311 AA;  
SQ  
Query Match 100.0%; Score 1644; DB 2; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.4e-164;  
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOTFTWVLEIWTSLFMWFFYALIPCLLTDEVAIIPAPONLSVLSTNMKHLWMSVIAP 60  
DB 1 MOTFTWVLEIWTSLFMWFFYALIPCLLTDEVAIIPAPONLSVLSTNMKHLWMSVIAP 60  
QY 61 GETVYVSVEYQGEYSLYTSHIWIWSSWCSLTEGPECVTDITATVPYNLRVRLGSG 120  
DB 61 GETVYVSVEYQGEYSLYTSHIWIWSSWCSLTEGPECVTDITATVPYNLRVRLGSG 120  
QY 121 TSAMSLKHPPNRSNLTILTRPGMEITKOGFHLVIELEDLGPQFEFLVAYVRREPGEAEHV 180  
DB 121 TSAMSLKHPPNRSNLTILTRPGMEITKOGFHLVIELEDLGPQFEFLVAYVRREPGEAEHV 180  
QY 181 KMRSGGIPVHLETWEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAP 240  
DB 181 KMRSGGIPVHLETWEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAP 240  
QY 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPOKLLISCRREEVDACATVM 300  
DB 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPOKLLISCRREEVDACATVM 300  
QY 301 SPEELLRAWIS 311  
DB 301 SPEELLRAWIS 311  
RESULT 2  
AA466676  
ID AA466676 standard; protein; 311 AA.  
XX  
XX AA466676;  
XX  
XX 05-APR-2000 (first entry)  
DT  
XX Membrane-bound protein PRO1114.  
DE  
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
KW  
XX Homo sapiens.  
OS  
XX WO9963088-A2.  
PN  
XX 09-DEC-1999.  
PD  
XX 02-JUN-1999; 99WO-US012252.  
PF  
XX 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
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PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
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PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088722P.  
PR 10-JUN-1998; 98US-0088730P.  
PR 10-JUN-1998; 98US-0088734P.  
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PR 10-JUN-1998; 98US-0088810P.  
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PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088825P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088863P.  
PR 12-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089090P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 18-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
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PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089947P.  
PR 19-JUN-1998; 98US-0089948P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
PR 23-JUN-1998; 98US-0090349P.  
PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090445P.  
PR 24-JUN-1998; 98US-0090461P.  
PR 24-JUN-1998; 98US-0090472P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090538P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 25-JUN-1998; 98US-0090557P.  
PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090688P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090691P.  
PR 25-JUN-1998; 98US-0090694P.  
PR 25-JUN-1998; 98US-0090695P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091358P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091486P.

PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 30-JUL-1998; 98US-0093339P.  
PR 04-AUG-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095285P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
PR 04-AUG-1998; 98US-0095318P.  
PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
PR 10-AUG-1998; 98US-0095916P.  
PR 10-AUG-1998; 98US-0095929P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
PR 17-AUG-1998; 98US-0096791P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096894P.  
PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097951P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0106634P.  
PR 12-JAN-1999; 99US-0115565P.

(GETH ) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX WPI; 2000-072883/06.  
XX N-PSDB; AA265011.

Membrane-bound proteins and related nucleotide sequences.

Claim 12; Fig 117; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and  
XX polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO

CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques  
XX  
XX Sequence 311 AA;

Query Match 100.0%; Score 1644; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.4e-164;  
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOTFTWVLEIWTSLPMWFYALIPCLLTDEVAIIPAPONLSVLSTNMKHLWSPVIAP 60  
DB 1 MOTFTWVLEIWTSLPMWFYALIPCLLTDEVAIIPAPONLSVLSTNMKHLWSPVIAP 60  
QY 61 GETVYVSVEYQGEYSLYTSHTIWPSSWCSTEGPECDVTDDITATVPYNLRVATLGSQ 120  
DB 61 GETVYVSVEYQGEYSLYTSHTIWPSSWCSTEGPECDVTDDITATVPYNLRVATLGSQ 120  
QY 121 TSAWSILKHPFRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGEAEHV 180  
DB 121 TSAWSILKHPFRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGEAEHV 180  
QY 181 KWRSGGIPVHLETMEPGAAVCVKAQTFVKAIGRVSFAFSQTECVQGEAIPLVLALFAF 240  
DB 181 KWRSGGIPVHLETMEPGAAVCVKAQTFVKAIGRVSFAFSQTECVQGEAIPLVLALFAF 240  
QY 241 VGFMLILVVVPLFVWKMGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300  
DB 241 VGFMLILVVVPLFVWKMGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300  
QY 301 SPEELLRAWIS 311  
DB 301 SPEELLRAWIS 311

RESULT 3  
AAB33440  
ID AAB33440 standard; protein; 311 AA.  
XX  
XX AAB33440;  
XX  
XX 29-JAN-2001 (first entry)  
XX  
XX Human PRO1114 protein UNQ557 SEQ ID NO:144.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; neutropic; neuroprotective;  
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease.

OS Homo sapiens.  
XX  
XX WO200053758-A2.  
XX  
XX 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US005841.  
PF  
XX 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99US-0123618P.  
PR 12-MAR-1999; 99US-0123957P.  
PR 23-MAR-1999; 99US-0125775P.  
PR 12-APR-1999; 99US-0128849P.  
PR 20-APR-1999; 99WO-US0008615.  
PR 28-APR-1999; 99US-0131445P.  
PR 04-MAY-1999; 99US-0132371P.  
PR 14-MAY-1999; 99US-0134287P.  
PR 23-JUN-1999; 99US-014037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-OCT-1999; 99US-0162506P.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 11-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
Karakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

WPI: 2000-572271/53.  
N-PSDB; AAC58605.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33; Fig 54; 309pp; English.

The present invention describes sixty four human PRO proteins which can  
be used in the treatment of immune related diseases. The human PRO  
proteins, anti-PRO antibodies, agonists and antagonists are useful for  
treating and diagnosing immune related disorders. The disorders are  
selected from systemic lupus erythematosus, rheumatoid arthritis,  
osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central and  
peripheral nervous systems, hepatobiliary diseases, inflammatory bowel  
disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune  
or immune-mediated skin diseases, allergic diseases, immunological  
diseases of the lung, and transplantation associated diseases including  
graft rejection and graft-versus-host-disease. AAC58397 to AAC58578

CC	represent PCR primers and hybridisation probes used in the isolation of
CC	human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC	represent human PRO polynucleotide and protein sequences given in the
CC	exemplification of the present invention
XX	
SQ	Sequence 311 AA;
	Query Match            100.0%; Score 1644; DB 3; Length 311;
	Best Local Similarity   100.0%; Pred. No. 1.4e-164;
	Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MOTFTMWLEETWTSLEFWFFYALIPCLLTDEVAILLPAPONLSVLSTNNKHLMMSPVIAP 60 
Dd	1 MOTFTMWLEETWTSLEFWFFYALIPCLLTDEVAILLPAPONLSVLSTNNKHLMMSPVIAP 60 
QY	61 GETVYVEYQGEYESLYTSHIWPSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQ 120 
Dd	61 GETVYVEYQGEYESLYTSHIWPSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQ 120 
QY	121 TSAMSIILKHPNRNSTILTRPGMEITKDGFHLVILEDLGQPQFELVAYWRREPGEAHHV 180 
Dd	121 TSAMSIILKHPNRNSTILTRPGMEITKDGFHLVILEDLGQPQFELVAYWRREPGEAHHV 180 
QY	181 KMRSGGIPVHLETMETPCAAACVKQAOTFKVKAIGRYSAFSQTECQEVOGEAIPLVIALPAF 240 
Dd	181 KMRSGGIPVHLETMETPCAAACVKQAOTFKVKAIGRYSAFSQTECQEVOGEAIPLVIALPAF 240 
QY	241 VGFMLLIIVVPLFWKMGRILOYSCCPVVLPDCLKITNSPKQLISCRREVDACATAVM 300 
Dd	241 VGFMLLIIVVPLFWKMGRILOYSCCPVVLPDCLKITNSPKQLISCRREVDACATAVM 300 
QY	301 SPELLRAWIS 311 
Dd	301 SPELLRAWIS 311 
RESULT 4	
AAY44664	ID ID AAY44664 standard; protein; 311 AA.
XX	
AC	AAY44664;
XX	
XX	18-APR-2000 (first entry)
XX	
DE	Interferon Receptor-HKAEF92.
XX	
KW	Interferon receptor HKAEF92; INFR; ATCC No. 209746; viral infection;
KW	immune dysfunction; immune system disorder; proliferative disease;
KW	cancer; inflammatory disorder; persistent infection; autoimmune disease;
KW	arthritis; leukemia; lymphoma; immunosuppression; myelosuppression;
KW	inflammatory bowel disease; Jaks-STATS signal transduction pathway.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Peptide 1..19
FT	/label= Signal_peptide
FT	Peptide 69..77
FT	/note= "Antigenic epitope-bearing peptide"
FT	Peptide 92..107
FT	/note= "Antigenic epitope-bearing peptide"
FT	Peptide 129..162
FT	/note= "Antigenic epitope-bearing peptide"
FT	Domain 130..233
FT	/label= Extracellular_domain
FT	Peptide 172..199
FT	/note= "Antigenic epitope-bearing peptide"
FT	Domain 234..250
FT	/label= Transmembrane_domain
FT	Domain 251..311
FT	/label= Intracellular_domain
FT	Peptide 272..307
FT	/note= "Antigenic epitope-bearing peptide"







Db 1 MOTFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLMLWSPVIAP 60  
QY 61 GETVYYSVEYQGEYSLYTSHIWIPSSWCSLSTEGPECDDTDDITATVPYNLRVRATLGSQ 120  
Db 61 GETVYYSVEYQGEYSLYTSHIWIPSSWCSLSTEGPECDDTDDITATVPYNLRVRATLGSQ 120  
QY 121 TSAMSLKHPPFNRRNSTILTRPGMEITKDGFLHVLIELEDLGPOPEFLVAYVRREPGEAEHV 180  
Db 121 TSAMSLKHPPFNRRNSTILTRPGMEITKDGFLHVLIELEDLGPOPEFLVAYVRREPGEAEHV 180  
QY 181 KMYRSGGIPVHLETMPEPGAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLLALFAP 240  
Db 181 KMYRSGGIPVHLETMPEPGAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLLALFAP 240  
QY 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300  
Db 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300  
QY 301 SPEELLRAWIS 311  
Db 301 SPEELLRAWIS 311  
RESULT 8  
AAB85270  
ID AAB85270 standard; protein; 311 AA.  
XX AAB85270;  
XX AAB85270;  
DT 07-SEP-2001 (first entry)  
DE Human IL-20 receptor subunit IL-20RB.  
KW Interleukin 20; IL-20; IL-20RA; Zcytor7; IL-20RB; DIRS1; immunoglobulin;  
KW antiinflammatory; anipsoiratic; antiasthmatic; antibacterial; human;  
KW dermatological; antiulcer; antagonist.  
XX Homo sapiens.  
XX WO200146232-A2.  
XX 28-JUN-2001.  
XX 22-DEC-2000; 2000WO-US035307.  
XX 23-DEC-1999; 99US-00471774.  
XX 22-JUN-2000; 2000US-0213416P.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;  
PI Rixon MW, Preenell SR, Fox BA,  
XX WPI; 2001-398320/42.  
DR N-PSDB; AAB22816.  
XX Isolated interleukin 20 soluble receptor comprising two polypeptide  
PT subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus  
PT treating inflammatory diseases such as psoriasis.  
XX Example 2; Page 68-69; 119pp; English.  
XX The invention relates to an interleukin 20 (IL-20) soluble receptor  
CC comprising two polypeptide subunits IL-20RA (formerly known as Zcytor7)  
CC and IL-20RB (formerly known as DIRS1). The two subunits are preferably  
CC linked together. In one embodiment, one subunit is fused to the constant  
CC region of the light chain of an immunoglobulin, and the other subunit is  
CC fused to constant region of the heavy chain of an immunoglobulin. The  
CC light chain and the heavy chain are connected via a disulphide bond. The  
CC soluble receptor can be used to down-regulate IL-20 and thus treat  
CC inflammatory diseases such as psoriasis, inflammatory lung injury such as  
CC asthma or bronchitis, adult respiratory disease (ARD), septic shock,  
CC multiple organ failure, bacterial pneumonia, eczema, atopic and contact

CC dermatitis, and inflammatory bowel disease such as ulcerative colitis and  
CC Crohn's disease. The present sequence represents a human IL-20 receptor  
CC subunit IL-20RB  
XX Sequence 311 AA;  
SQ Query Match 100.0%; Score 1644; DB 4; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.4e-164;  
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOTFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLMLWSPVIAP 60  
Db 1 MOTFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLMLWSPVIAP 60  
QY 61 GETVYYSVEYQGEYSLYTSHIWIPSSWCSLSTEGPECDDTDDITATVPYNLRVRATLGSQ 120  
Db 61 GETVYYSVEYQGEYSLYTSHIWIPSSWCSLSTEGPECDDTDDITATVPYNLRVRATLGSQ 120  
QY 121 TSAMSLKHPPFNRRNSTILTRPGMEITKDGFLHVLIELEDLGPOPEFLVAYVRREPGEAEHV 180  
Db 121 TSAMSLKHPPFNRRNSTILTRPGMEITKDGFLHVLIELEDLGPOPEFLVAYVRREPGEAEHV 180  
QY 181 KMYRSGGIPVHLETMPEPGAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLLALFAP 240  
Db 181 KMYRSGGIPVHLETMPEPGAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLLALFAP 240  
QY 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300  
Db 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300  
QY 301 SPEELLRAWIS 311  
Db 301 SPEELLRAWIS 311  
RESULT 9  
AAE00339  
ID AAE00339 standard; protein; 311 AA.  
XX AAE00339;  
XX AAE00339;  
DT 19-JUN-2001 (first entry)  
XX Human cytokine receptor protein, CG92.  
XX Human; cytokine receptor protein; CG92; antiinflammatory; antimicrobial;  
KW immunosuppressive; blood coagulation disorder; antidiabetic; cytostatic;  
KW gastrointestinal; acute pancreatitis; glomerulonephritis; gene therapy;  
KW severe combined immunodeficiency; SCID; autoimmune disorder; thrombosis;  
KW multiple sclerosis; rheumatoid arthritis; Alzheimer's disease; xenograft;  
KW graft versus host disease; GVHD; inflammatory bowel disease; haemostatic;  
KW endotoxin shock; psoriasis; osteoporosis; hepatitis; vascular; allograft;  
KW cell proliferative; haematopoietic; vasculitis; lupus; leukaemia; cancer;  
KW sarcoidosis; sepsis.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Key 1..29 /label= Signal\_peptide  
FT Peptide 30..311  
FT Protein /label= Mature\_human.CG92\_protein  
FT Region 35..224 /note= "Tissue factor structure region"  
FT Region 39..57 /label= Tissue\_factor\_signature  
FT Region 40..226 /note= "Tissue factor structure region"  
FT Domain 84..119 /label= Tissue\_factor\_domain  
FT Region 235..255 /note= "Shows high homology to bacterial chemotaxis  
FT sensory transducer signature"

XX WO200123569-A1.  
 XX PN  
 XX PD  
 XX PF 05-APR-2001.  
 XX PR 29-SEP-2000; 2000WO-US026850.  
 XX PR 29-SEP-1999; 99US-00408027.  
 XX PA (HYSB-) HYSEQ INC.  
 XX PI Ballinger D, Ford J, Pace A, Sheridan J;  
 XX DR WPI; 2001-266162/27.  
 XX DR N-PSDB; AAD03547.  
 XX PT Polynucleotides encoding human cytokine receptor CG92, useful for  
 XX PT preventing, diagnosing and treating inflammation and disorders of blood  
 XX PT coagulation.  
 XX PS Claim 10; Fig 1-3; 109pp; English.  
 XX CC The present sequence is human cytokine receptor protein, designated as  
 CC CG92. CG92 is a member of the class II cytokine receptor (CRF2) family,  
 CC which includes R1 and R2 of chains of the IL-10 receptor complex. IFN-  
 CC alpha receptor complex, and tissue factor (TF). CG92 DNA and proteins are  
 CC used in the prevention, diagnosis and treatment of diseases associated  
 CC with inappropriate cytokine receptor expression such as inflammatory  
 CC disorders and disorders of blood coagulation. These disorders include  
 CC sepsis, thrombosis, acute pancreatitis, arthritis, vasculitis, lupus,  
 CC immune complex glomerulonephritis, diabetes, allograft and xenograft  
 CC transplantation, hepatitis, stroke and cancers. It is also used for  
 CC treating various immune deficiencies and disorders such as severe  
 CC combined immunodeficiency (SCID) and autoimmune disorders such as  
 CC multiple sclerosis, rheumatoid arthritis; nervous system disorders (e.g.,  
 CC Alzheimer's disease); sarcoidosis; leukemias (e.g., erythroleukaemia);  
 CC inflammations such as graft versus host disease (GVHD) inflammatory  
 CC bowel disease and endotoxin shock; hyperproliferative disorders (e.g.,  
 CC psoriasis); cancers (e.g., non-Hodgkin's lymphoma, prostate cancer) and  
 CC bone degenerative diseases such as osteoporosis. CG92 cDNA is also used  
 CC in gene therapy. CG92 possesses cytokine and cell  
 CC proliferation/differentiation activity, immune regulating activity,  
 CC haematopoiesis regulating activity, tissue growth activity, haemostatic  
 CC and thrombolytic activity, receptor/ligand activity and anti-inflammatory  
 CC activity. CG92 is also used in assays to identify modulators of cytokine  
 CC receptor expression and their activities  
 XX SQ Sequence 311 AA;  
 Query Match 100.0%; Score 1644; DB 4; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-164;  
 Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQFTWVLEIWTSLFWFFYALIPCLLTDEVAIPAPQNLISVLSTNMKHLWSPVIAP 60  
 DB 1 MQFTWVLEIWTSLFWFFYALIPCLLTDEVAIPAPQNLISVLSTNMKHLWSPVIAP 60  
 QY 61 GETVYISVEYQGVESLYTSHIWPSSWCSLTGPECDDTDDITATVPYNLRVATLGSQ 120  
 DB 61 GETVYISVEYQGVESLYTSHIWPSSWCSLTGPECDDTDDITATVPYNLRVATLGSQ 120  
 QY 121 TSWSILKHPFNRRNLTITPGMEITKDGPHLVIELEDLGPQFEFLVAYWRPFGAEHV 180  
 DB 121 TSWSILKHPFNRRNLTITPGMEITKDGPHLVIELEDLGPQFEFLVAYWRPFGAEHV 180  
 QY 181 KMYRSGGIPVHLEMTBEGGAYCVKAOFTVKAIGRYSAFSQTECVQGEAIPLVLALFAF 240  
 DB 181 KMYRSGGIPVHLEMTBEGGAYCVKAOFTVKAIGRYSAFSQTECVQGEAIPLVLALFAF 240  
 QY 241 VGFMLILVVVPLFWKMGRLLOYSCEPVVLPDTLKITNSPQKLISCRREEVDACATVM 300  
 DB 241 VGFMLILVVVPLFWKMGRLLOYSCEPVVLPDTLKITNSPQKLISCRREEVDACATVM 300

QY 301 SPEELLRAWIS 311  
 DB 301 SPEELLRAWIS 311  
 RESULT 10  
 AAU04059  
 ID AAU04059 standard; protein; 311 AA.  
 XX AC AAU04059;  
 XX DT 23-OCT-2001 (first entry)  
 XX DE Human interleukin-20 receptor B, IL-20RB.  
 XX KW Human; interleukin-20 receptor B; IL-20RB; antagonist; psoriasis; eczema;  
 KW dermatitis; adult respiratory disease; asthma; bronchitis; pneumonia;  
 KW multiple organ failure; inflammatory lung injury; septic shock;  
 KW bacterial pneumonia; inflammatory bowel disease; rheumatoid arthritis;  
 KW ulcerative colitis; Crohn's disease.  
 XX OS Homo sapiens.  
 XX FH Key  
 FT Peptide 1..29 /label= Signal\_peptide  
 FT Protein 30..311 /label= Mature\_IL-20RB  
 FT Domain 30..232 /label= Extracellular\_domain  
 XX WO200146261-A1.  
 XX 28-JUN-2001.  
 XX 22-DEC-2000; 2000WO-US035305.  
 XX 23-DEC-1999; 99US-00470898.  
 XX 22-JUN-2000; 2000US-0213341P.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Thompson P, Foster DC, Wenfeng X, Madden KL, Kelly JD;  
 PI Sprecher CA, Blumberg H, Eagan MA, Jaspers SR, Chandrasekhar JA;  
 PI Novak JE;  
 XX WPI; 2001-418045/44.  
 DR N-PSDB; AAS07644.  
 XX Treating interleukin-20 induced inflammation in a mammal, such as adult  
 PT respiratory disease, eczema, psoriasis, contact dermatitis, multiple  
 PT organ failure and septic shock, involves administering IL-20 antagonist.  
 XX Example 2; Page 62-63; 117pp; English.  
 PS The sequence represents the Human interleukin-20 receptor B, IL-20RB. The  
 XX invention relates to treating a mammal afflicted with a disease in which  
 CC an interleukin-20 (IL-20) polypeptide plays a role, involves  
 CC administering antagonist of IL-20 polypeptide to the individual. The  
 CC method is useful for treating psoriasis, eczema, atopic dermatitis,  
 CC contact dermatitis, adult respiratory disease, asthma, bronchitis and  
 CC pneumonia and is also useful for treating multiple organ failure,  
 CC inflammatory lung injury, septic shock, bacterial pneumonia, inflammatory  
 CC bowel disease, rheumatoid arthritis, ulcerative colitis and Crohn's  
 CC disease  
 XX Sequence 311 AA;  
 QY Query Match 100.0%; Score 1644; DB 4; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-164;  
 Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQFTWVLEIWTSLFWFFYALIPCLLTDEVAIPAPQNLISVLSTNMKHLWSPVIAP 60

Db 1 MQTFTVLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSPIAP 60  
Qy 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120  
Db 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120  
Qy 121 TSAWSILKHPFNRSNLTIRPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV 180  
Db 121 TSAWSILKHPFNRSNLTIRPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV 180  
Qy 181 KMRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240  
Db 181 KMRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240  
Qy 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAM 300  
Db 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAM 300  
Qy 301 SPEELLRAWIS 311  
Db 301 SPEELLRAWIS 311  
RESULT 11  
ID AAB65199  
XX AAB65199 standard; protein; 311 AA.  
AC AAB65199;  
XX  
DT 02-APR-2001 (first entry)  
TX Human PRO1114 (UNQ557) protein sequence SEQ ID NO:183.  
DE Human; secreted and transmembrane protein; PRO; cytostatic; cell death;  
XX cancer; chromosomal mapping; Gene mapping; tissue typing;  
KW diagnostic assay.  
KW Homo sapiens.  
OS  
XX WO200073454-A1.  
PN  
XX 07-DEC-2000.  
PD  
XX 30-MAR-2000; 2000WO-US008439.  
PF  
XX 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 18-OCT-1999; 99US-0158663P.  
PR 08-NOV-1999; 99WO-US026313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US005884.  
PR 20-MAR-2000; 2000WO-US007377.  
XX  
XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Deanoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
XX Zhang Z;  
DR WPI; 2001-032160/04.  
DR N-PSDB; AAF44157.  
XX  
PT PRO polynucleotides used to produce polypeptides used to target bioactive  
PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
XX to cause targeted cell death.  
XX  
PS Claim 12; Fig 117; 935pp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
CC be used for targeted delivery of bioactive molecules, such as toxins,  
CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
CC DNA. They may also be used to produce transgenic animals which are used  
CC to develop and screen therapeutically useful reagents. The PRO nucleotide  
CC and protein sequence can be used for tissue typing and in treating  
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
CC AAF44470 represent PCR primers and hybridisation probes used in the  
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to  
CC AAB65300 represent human PRO polynucleotide and protein sequences given  
CC in the exemplification of the present invention  
XX  
SQ Sequence 311 AA;  
Query Match 100.0%; Score 1644; DB 4; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.4e-164;  
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQTFTVLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSPIAP 60  
Db 1 MQTFTVLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSPIAP 60  
Qy 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120  
Db 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120  
Qy 121 TSAWSILKHPFNRSNLTIRPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV 180  
Db 121 TSAWSILKHPFNRSNLTIRPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV 180  
Qy 181 KMRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240  
Db 181 KMRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240  
Qy 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAM 300  
Db 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAM 300  
Qy 301 SPEELLRAWIS 311  
Db 301 SPEELLRAWIS 311  
RESULT 12  
ID AAB67201  
XX AAB67201 standard; protein; 311 AA.  
AC AAB67201;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Human interleukin-20 sub-unit IL20RB.  
XX  
KW Inflammation; interleukin-20; IL-20; interleukin-8; IL-8; chemokine;  
KW neutrophil; monocyte; basophil; eosinophil; chemoattractant; psoriasis;

periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis; angiogenesis-dependent chronic inflammatory condition; lung cancer; melanoma; inflammatory disease; diabetes; arteriosclerosis; cataract; reperfusion injury; cancer; meningitis; rheumatic disease; skin disease; idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis; ulcerative colitis; eczema; atopic dermatitis; contact dermatitis; inflammatory lung disease; ARD; adult respiratory disease; asthma; bronchitis; pneumonia.

OS Homo sapiens.

PN US2002042366-A1.

PD 11-APR-2002.

XX 22-DEC-2000; 2000US-00746359.

XX 23-DEC-1999; 99US-0171969P.

PR 22-JUN-2000; 2000US-0213341P.

XX (THOM/) THOMPSON P.

PA (POST/) FOSTER D C.

PA (XUW/) XU W.

PA (MADD/) MADDEN K L.

PA (KELL/) KELLY J D.

PA (SPRE/) SPRECHER C A.

PA (BLUM/) BLUMBERG H.

PA (BAGA/) BAGAN M A.

PA (JASP/) JASPERS S R.

PA (CHAN/) CHANDRASEKHAR Y A.

PA (NOVA/) NOVAK J E.

XX Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA; Blumberg H, Bagan MA, Jaspers SR, Chandrasekhar YA, Novak JE; PI

PI WPI: 2002-507215/54.

XX N-PSDB; ABK96177.

DR

DR

XX Treating inflammatory skin and lung diseases using antibodies against interleukins (IL)-20 (which indirectly modulates activation of IL-8), useful for treating e.g. psoriasis, asthma and bronchitis.

PS Example 2; Page 23-24; 68pp; English.

XX The invention describes a method (I) for treating a mammal afflicted with a disease in which an interleukin-20 (IL-20) polypeptide plays a role comprising administering antagonist of the IL-20 polypeptide to the individual. An important cytokine in the inflammatory process is interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils via chemotaxis and the release of granule enzymes. IL-8 binds to receptors on neutrophils, monocytes, basophils, and eosinophils. IL-8 is a potent chemoattractant for neutrophils; and the early stages of periodontal disease are characterized by the influx of neutrophils. IL-8 is a potent inducer of angiogenesis in several angiogenesis-dependent chronic inflammatory conditions, including rheumatoid arthritis, psoriasis, and idiopathic pulmonary fibrosis. Additionally, IL-8 is an important source of angiogenic activity in human lung cancer. Also, IL-8 expression correlates with experimental metastatic activity of some melanoma cell lines. Therefore an effective method to treat inflammatory diseases would be to administer an agent that would inhibit IL-8. It has been shown that IL-20 up-regulates IL-8. Therefore antagonists to IL-20 can be used to treat these diseases. The method is used for treating diseases in which the IL-20 polypeptide plays a role e.g. inflammatory diseases including diabetes, arteriosclerosis, cataracts, reperfusion injury, cancer, meningitis, rheumatic diseases, idiopathic pulmonary fibrosis, inflammatory bowel disease (ulcerative colitis), skin disease (psoriasis), eczema, atopic dermatitis and contact dermatitis) or an inflammatory lung disease (adult respiratory disease (ARD), asthma, bronchitis and pneumonia). This sequence represents a human interleukin-20 (IL-20) polypeptide used in developing the method of the invention

XX Sequence 311 AA;

Query Match 100.0%; Score 1644; DB 5; Length 311;  
Best Local Similarity 100.0%; Pred. No. 1.4e-164;  
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQTFTVBLEIWTSLFPMFFYALIPCLLTDEVAIPAPQNLVSLTNMGLLWMSPIAP 60  
DB 1 MQTFTVBLEIWTSLFPMFFYALIPCLLTDEVAIPAPQNLVSLTNMGLLWMSPIAP 60

QY 61 GETVYYSVEYQGEYSIYTSIWIPISSWCSLTGSPCEDVTDITATVPYNLVRATILGSQ 120  
DB 61 GETVYYSVEYQGEYSIYTSIWIPISSWCSLTGSPCEDVTDITATVPYNLVRATILGSQ 120

QY 121 TSAWSILKHPPFNENSTILTRPGMEITKDGPHLVEILEDLGQFEFLVAYWRRPGEAEHV 180  
DB 121 TSAWSILKHPPFNENSTILTRPGMEITKDGPHLVEILEDLGQFEFLVAYWRRPGEAEHV 180

QY 181 KMRVSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECEVQGEAIPVLALFAF 240  
DB 181 KMRVSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECEVQGEAIPVLALFAF 240

QY 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVLPDTLKITNSPQKLISCRREEVACATAVM 300  
DB 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVLPDTLKITNSPQKLISCRREEVACATAVM 300

QY 301 SPEELLRAWIS 311  
DB 301 SPEELLRAWIS 311

RESULT 13  
ABB90182  
ID ABB90182 standard; protein; 311 AA.  
XX ABB90182;  
XX 24-MAY-2002 (first entry)  
XX Human polypeptide SEQ ID NO 2558.  
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer; vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiact; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.  
XX Homo sapiens.  
XX WO200190304-A2.  
XX 29-NOV-2001.  
XX 19-MAY-2001; 2001WO-US016450.  
XX 19-MAY-2000; 2000US-0205515P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Birse CE, Rosen CA;  
XX WPI: 2002-122018/16.  
XX N-PSDB; ABI90591.  
XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders.  
XX Claim 11; SEQ ID NO 2558; 2081pp + Sequence Listing; English.  
XX The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB9040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.

CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 311 AA;

Query Match 100.0%; Score 1644; DB 5; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-164;  
 Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSVPIAP 60  
 DB 1 MQFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSVPIAP 60  
 QY 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECVTDITATVPYNLRVRLTGSQ 120  
 DB 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECVTDITATVPYNLRVRLTGSQ 120  
 QY 121 TSAMSLKHPFNNSILTRPGMEITKDGPHLVIELEDLGPQEFVLVYWRREPGEAEHV 180  
 DB 121 TSAMSLKHPFNNSILTRPGMEITKDGPHLVIELEDLGPQEFVLVYWRREPGEAEHV 180  
 QY 181 KMYRSGGIPVHLETPMPEGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPLVLALFAP 240  
 DB 181 KMYRSGGIPVHLETPMPEGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPLVLALFAP 240  
 QY 241 VGFMILILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLIISCRREEVDACATAM 300  
 DB 241 VGFMILILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLIISCRREEVDACATAM 300  
 QY 301 SPEELLRAWIS 311  
 DB 301 SPEELLRAWIS 311

RESULT 14  
 AAE23355  
 ID AAE23355 standard; protein; 311 AA.  
 AC AAE23355;  
 XX  
 XX  
 XX  
 DT 27-AUG-2002 (first entry)

DE Human interleukin-20 receptor beta variant (V-IL-20RB) protein.  
 XX  
 XX Human; interleukin-19; IL-19; interleukin-20 receptor alpha; IL-20RA;  
 KW interleukin-20 receptor beta; IL-20RB; inflammation; atherosclerosis;  
 KW diabetes; reperfusion injury; cancer; infectious meningitis; cataract;  
 KW rheumatoid arthritis; rheumatic fever; systemic lupus erythematosus;  
 KW antibacterial; cytostatic; dermatological; ophthalmological; vasotropic;  
 KW variant.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1..29  
 FT /label= Signal\_peptide  
 FT 30..311  
 FT Protein  
 FT /note= "Human mature V-IL-20RB protein"

XX WO200222153-A2.

PD 21-MAR-2002.  
 XX  
 XX 13-SEP-2001; 2001WO-US028557.  
 XX  
 PR 15-SEP-2000; 2000US-0233305P.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Chandrasekher YA, Jaspers SR;  
 XX WPI; 2002-425815/45.  
 DR N-PSDB; AAD37555.  
 DR  
 XX  
 PT Method of down-regulating IL-19 useful for treating inflammation  
 PT comprises administration of a polypeptide comprised of the extracellular  
 PT domain of IL-20RA and IL-20RB.  
 XX  
 PS Disclosure; Page 50-51; 80pp; English.

XX  
 CC The present invention relates to a method of down-regulating interleukin  
 CC (IL)-19. The method involves administration of a polypeptide comprised of  
 CC the extracellular domain of interleukin-20 receptor alpha (IL-20RA) and  
 CC the extracellular domain of interleukin-20 receptor beta (IL-20RB). The  
 CC IL-20RA and IL-20RB are heterodimeric receptors that bind to both IL-19  
 CC and mda7. The method is useful for down-regulating IL-19, useful for the  
 CC treatment of inflammation e.g., in diabetes, atherosclerosis, cataracts,  
 CC reperfusion injury, cancer, infectious meningitis, rheumatoid arthritis,  
 CC rheumatic fever and systemic lupus erythematosus. The present sequence is  
 CC human IL-20RB variant (V-IL-20RB) protein

XX Sequence 311 AA;

Query Match 100.0%; Score 1644; DB 5; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-164;  
 Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSVPIAP 60  
 DB 1 MQFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSVPIAP 60  
 QY 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECVTDITATVPYNLRVRLTGSQ 120  
 DB 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECVTDITATVPYNLRVRLTGSQ 120  
 QY 121 TSAMSLKHPFNNSILTRPGMEITKDGPHLVIELEDLGPQEFVLVYWRREPGEAEHV 180  
 DB 121 TSAMSLKHPFNNSILTRPGMEITKDGPHLVIELEDLGPQEFVLVYWRREPGEAEHV 180  
 QY 181 KMYRSGGIPVHLETPMPEGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPLVLALFAP 240  
 DB 181 KMYRSGGIPVHLETPMPEGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPLVLALFAP 240  
 QY 241 VGFMILILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLIISCRREEVDACATAM 300  
 DB 241 VGFMILILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLIISCRREEVDACATAM 300  
 QY 301 SPEELLRAWIS 311  
 DB 301 SPEELLRAWIS 311

RESULT 15  
 ABB84877  
 ID ABB84877 standard; protein; 311 AA.  
 XX  
 AC ABB84877;  
 XX  
 DT 16-MAY-2002 (first entry)  
 XX  
 XX Human PRO1114 protein sequence SEQ ID NO:122.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.  
 XX  
 OS Homo sapiens.

XX

PN W0200200690-A2.

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gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 age-related macular degeneration; arterial restenosis; angina;  
 rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 wound healing; chromosome mapping; gene mapping.

Homo sapiens.

W0200200690-A2.

03-JAN-2002.

20-JUN-2001; 2001WO-US019692.

23-JUN-2000; 2000US-0213637P.

20-JUL-2000; 2000US-0219556P.

25-JUL-2000; 2000US-0220624P.

25-JUL-2000; 2000US-0220664P.

28-JUL-2000; 2000WO-US020710.

02-AUG-2000; 2000US-0222859P.

17-AUG-2000; 2000US-00643657.

23-AUG-2000; 2000WO-US023522.

24-AUG-2000; 2000US-0230978P.

07-SEP-2000; 2000US-00664610.

18-SEP-2000; 2000US-00663550.

24-OCT-2000; 2000US-0242922P.

08-NOV-2000; 2000US-00709238.

08-NOV-2000; 2000WO-US030952.

10-NOV-2000; 2000WO-US030873.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.

20-DEC-2000; 2000WO-US034956.

22-JAN-2001; 2001US-00767609.

28-FEB-2001; 2001US-00796498.

28-FEB-2001; 2001WO-US006520.

01-MAR-2001; 2001WO-US008666.

09-MAR-2001; 2001US-00802706.

14-MAR-2001; 2001US-00808689.

22-MAR-2001; 2001US-00816744.

05-APR-2001; 2001US-00828366.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854280.

25-MAY-2001; 2001US-00866028.

25-MAY-2001; 2001US-00866034.

30-MAY-2001; 2001WO-US017092.

30-MAY-2001; 2001US-00870574.

30-MAY-2001; 2001WO-US017443.

01-JUN-2001; 2001WO-US017800.

(GETH ) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerecht H, Goddard A;  
 Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.

N-PSDB; ABL88132.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 infarction), endothelial or angiogenic disorders in a mammal.

Claim 11; Fig 122; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABL84817 to  
 ABL85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 activities, and can be used in gene therapy. The PRO polynucleotides,  
 proteins, agonists and antagonists are useful for treating or diagnosing  
 a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
 cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The PRO polynucleotides have applications in molecular biology,  
 CC including use as hybridisation probes, and in chromosome and gene  
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
 CC exemplification of the present invention

XX Sequence 311 AA;

Query Match	100.0%;	Score 1644;	DB 5;	Length 311;
Best Local Similarity	100.0%;	Pred. No. 1.4e-164;		
Matches 311;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MQTFTMVLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLSTNMKHLMLWSPVIAP	60	
Db	1	MQTFTMVLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLSTNMKHLMLWSPVIAP	60	
QY	61	GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDDITATVPYNLVRATLGSQ	120	
Db	61	GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDDITATVPYNLVRATLGSQ	120	
QY	121	TSAWSILKHPFNRNSTILTRPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV	180	
Db	121	TSAWSILKHPFNRNSTILTRPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV	180	
QY	181	KMVRSGGIPVHLETPMEPGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPVLALPAF	240	
Db	181	KMVRSGGIPVHLETPMEPGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPVLALPAF	240	
QY	241	VGFMILILVVPLFVWKMGRLLQYSCCPVVLPDTLKITNSPKKLISCRREEVDACATVM	300	
Db	241	VGFMILILVVPLFVWKMGRLLQYSCCPVVLPDTLKITNSPKKLISCRREEVDACATVM	300	
QY	301	SPEELLRAWIS 311		
Db	301	SPEELLRAWIS 311		

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Job time : 121.705 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: April 5, 2006, 11:36:04 ; Search time 18.3576 Seconds  
(without alignments)  
1630.025 Million cell updates/sec

Title: US-09-745-792A-14  
Perfect score: 1644  
Sequence: 1 MDTFTWLEIWTSLFWWFF.....VDACATVMSPELLRAWIS 311

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: Pirl:\*  
2: Pirl:\*  
3: Pirl:\*  
4: Pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	12.4	325	2 A47003	Cytokine receptor
2	189.5	11.5	590	2 A45283	interferon alpha/b
3	188.5	11.5	337	2 I38500	interferon gamma r
4	183.5	11.2	349	2 JC6311	interferon recepto
5	181.5	11.0	560	2 S27387	interferon alpha r
6	173.5	10.6	557	2 A32694	interferon alpha/b
7	163	9.9	332	2 A49947	interferon gamma r
8	148	9.0	578	2 I56215	interleukin-10 rec
9	139	8.5	292	1 KFRB3	tissue factor prec
10	132.5	8.1	295	1 KFHU3	tissue factor prec
11	129.5	7.9	575	2 A49667	interleukin-10 rec
12	126.5	7.7	294	1 KFM53	tissue factor prec
13	122	7.4	489	2 A31555	interferon gamma r
14	117.5	7.1	292	1 KFB03	tissue factor prec
15	111	6.8	507	1 A32385	erythropoietin rec
16	103.5	6.3	1118	1 A49724	protein-tyrosine-p
17	101.5	6.2	419	2 T10652	hypothetical prote
18	96	5.8	507	1 A46713	erythropoietin rec
19	96	5.8	984	2 A39753	protein-tyrosine k
20	95	5.8	896	2 I56563	interleukin-3 rece
21	94.5	5.7	359	2 S55653	hypothetical prote
22	94	5.7	508	1 ZUHUR	erythropoietin rec
23	93.5	5.7	1427	2 I51669	tumor suppressor r
24	93	5.7	1447	2 A54100	tumor suppressor p
25	92	5.6	379	2 S56193	probable membrane
26	92	5.6	977	2 S49004	tyrosine kinase Mp
27	92	5.6	2311	1 TVCHSR	kinase-related pro
28	91.5	5.6	987	2 A54092	protein-tyrosine k
29	89.5	5.4	567	2 F81682	phosphoenolpyruvat

30	89	5.4	985	2 I51549	receptor tyrosine
31	87.5	5.3	896	1 A35782	cytokine receptor
32	87.5	5.3	1328	2 JS0610	beta-galactosidase
33	87	5.3	831	2 JQ1655	prolactin receptor
34	86	5.2	952	2 I50612	protein-tyrosine k
35	86	5.2	227	2 I37081	cytochrome-c oxida
36	86	5.2	227	2 T11483	cytochrome-c oxida
37	86	5.2	549	2 S74467	hypothetical prote
38	85.5	5.2	245	2 G87801	protein C10G11.4
39	85.5	5.2	1557	2 D41214	protein-tyrosine-p
40	85.5	5.2	1630	2 C41214	protein-tyrosine-p
41	85	5.2	227	2 T11250	cytochrome-c oxida
42	85	5.2	227	2 T11053	cytochrome-c oxida
43	85	5.2	265	2 S14081	erythropoietin rec
44	85	5.2	495	2 H69614	aldehyde dehydroge
45	84.5	5.1	454	2 T20829	probable serine ca

ALIGNMENTS

RESULT 1

A47003  
cytokine receptor family class II protein CRF2-4 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C:Accession: A47003, G01418  
R:Lutfalla, G.; Gardiner, K.; Uze, G.  
Genomics 16, 366-373, 1993  
A>Title: A new member of the cytokine receptor gene family maps on chromosome 21 at less  
A:Reference number: A47003; MUID:93300510; PMID:8314576  
A:Accession: A47003  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Cross-references: 1-325 <LUT>  
A:Residues: 1-123,'D',125-268,'VGRME', <LU2>  
R:Lutfalla, G.  
submitted to the EMBL Data Library, April 1994  
A:Reference number: G06935  
A:Accession: G01418  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-123,'D',125-268,'VGRME', <LU2>  
A:Cross-references: UNIPARC:UPI000016A09D; EMBL:U08988; NID:g571295; PID:g571296

Query Match	12.4%;	Score	204;	DB 2;	Length	325;	
Best Local Similarity	27.1%;	Pred. No.	2.7e-10;				
Matches	79;	Conservative	47;	Mismatches	113;	Gaps	17;
Qy	12	WTSLEWFFFYALIPCLLTDSVAILLPAPONLSVLSTNNKHLIMW-SPVIAPGEVTVYSVEY	70				
Db	3	W-SLGSW----LGGCLLVSGALGVPPPPVNRVNSVNFKNILQWESPAFAG-----NLTF	52				
Qy	71	QGEYESLYTSHIWPSSWCSLTGEGPCDVTDDITATVPYNLRVRLTGSQTSAM-SILKH	129				
Db	53	TQAQYLSYR----IFQDKCMNTTLTECDFS-SLSKYGDHTLRVRAEFADEHSDWNIITFC	106				
Qy	130	PFNRNSTILTRPGM--EITKDGPHLVIELEDLGQPE-----FLAVAYWR	171				
Db	107	PV--DDTIIGPGCMQVEVLADSLH---MRFLAPKIENEYETWTMKVNSWTVNYQYWK	160				
Qy	172	REPBAEHVMVRSGGIPVHLETMPECAAYCVKAQTFVKAIGRYSAFSQTECVS-VQGEA	230				
Db	161	N--GTDEKQITQYDFEV-LRNLEPWTTCVQVRGFLPDRNKAGSEWPVCEQITTHDET	217				
Qy	231	IP---LVTLALFAFVGFMJLILVVPLF--VWKGRLQLQYSCCPVVVLPTLTK	276				



C;Accession: JC6311  
R;Gibbs, V.C.; Pennica, D.  
Gene 186, 97-101, 1997  
A;Title: CRF2-4:Isolation of cDNA clones encoding the human and mouse proteins.  
A;Reference number: JC6311; MUID:97199375; PMID:9047351  
A;Accession: JC6311  
A>Status: preliminary  
A:Molecule type: mRNA  
A;Residues: 1-349 <GIB>  
A;Cross-references: UNIPROT:Q8VHM7; UNIPARC:UPI000017C6DE; GB:U53696

Query Match 11.2%; Score 183.5; DB 2; Length 349;  
Best Local Similarity 23.7%; Pred.No. 1.9e-08;  
Matches 68; Conservative 49; Mismatches 117; Indels 53; Gaps 13;

QY 23 LIPC-----LITDVAIILPAPQNLSVLSTNMKHLMMSPVIAPGETYYVSVEYQGEEY 74  
| | :  
Db 1 MAPCVAGWGGLLVLPALGMIPPEKVRMNSVNFKNILQWEVPAPFKTNLTFTAQYE-SY 59  
| | :  
QY 75 ESLYTSHIWIPSSWCSLTEGPCVDTDITATVPYNLRVRAITLGQSASW-SILKHPPNR 133  
| | :  
Db 60 RS-FQDH-----CKRTASTQCDFS-HLSKYGDYTVRVRAELADHSEHWNVTFCPV-- 108  
| | :  
QY 134 NSTILTPGMEITDKGHFLVLELDLGPQE-----FLVAYRRSPGAE 177  
| | :  
Db 109 EDTIIIGPENQI--ESLAESLEIRFSAPQIENBPETWTLNLYDSWAYRVQYWK--GTN 164  
| | :  
QY 178 EHVQRSGGIPVHLETMFGAAVCVKQAQTFVKAIGRYSAFSQTCEVQGE----- 229  
| | :  
Db 165 EKQVWSYDSEV-LRNLEPWTYTCIQOQLDONRTGWSESPICERTGNDEITPSWIV 223  
| | :  
QY 230 AILPLVALFAFVGFMILLVVVPLFVWRMGRLQLQVSCCPVVVLPDTLK 276  
| | :  
Db 224 AIILVSVLVLFLLGCFVV---LWLIYKKTKHTFRSGTSLFOHLK 267  
| | :

RESULT 5  
S27387  
interferon alpha receptor type 1 precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S27387; S33770  
R;Mouchel-Vieilh, B.; Luftalla, G.; Mogensen, K.E.; Uze, G.  
FEBS Lett. 313, 255-259, 1992  
A;Title: Specific antiviral activities of the human alpha interferons are determined at  
A;Reference number: S27387; MUID:93076908; PMID:1446745  
A;Accession: S27387  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A;Residues: 1-560 <MOU>  
A;Cross-references: UNIPROT:Q04790; UNIPARC:UPI000012D698; EMBL:X68443; NID:g431; PIDN:C  
A;Experimental source: MDBK cells  
R;Lim, J.K.; Langer, J.A.  
Biochim. Biophys. Acta 1173, 314-319, 1993  
A;Title: Cloning and characterization of a bovine alpha interferon receptor.  
A;Reference number: S33770; MUID:93305725; PMID:8318540  
A;Accession: S33770  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A;Residues: 1-421,'V',423-560 <LIW>  
A;Cross-references: UNIPARC:UPI0000167C2D; EMBL:L06320; NID:g163187; PIDN:AAA02571.1; P  
A;Experimental source: lung  
C;Keywords: antiviral; cytokine receptor; transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;23-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

Query Match 11.0%; Score 181.5; DB 2; Length 560;  
Best Local Similarity 22.9%; Pred.No. 5.2e-08;  
Matches 73; Conservative 62; Mismatches 133; Indels 51; Gaps 14;

QY 21 YALIPCLLTDEVAIILPAPQNLSVLSTNMKHLMMSPVIAPGETYYVSVEYQGESLYTS 80  
| | :  
Db 215 YSPVYCINTTRHKVPSFNPIONADNOIYVLKW-----DYPERATFOALRAFKK 267  
| | :

Qy	81	HI-----W-----IPSSWCSLTEGPECVDTDITATVPYNLRVRATLGSOTSAMSLKHDPF	131
Db	268	KIPGNHSDKWKQIEN--CENVYTHCVFPREVSSRGIYVVRASNGNGTSPWSEBKEFN	325
Qy	132	NRNSTILTRPGM--EITKDGFLHVI---ELEDLGPQ---FEFLVAYRRPEPGAEEHV	180
Db	326	TEMKTIFFPPVISUKSVTDDSLHVSVGASESENMSVNQLYPLIYEVIFWENTSNAERKV	385
Qy	181	KMVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRY--SAFSQTECVQVQ----GEAIPLV	234
Db	386	LEKRTNFI---FPDLKPLTVYCVKARALIENDRRNRKSGSFSDTVCEKTKPGNGTSKTWLI	442
Qy	235	LALFAFVGFMILIVVPLFVWKMGRLLQYSCPVVVLPTLTK--ITNSPOK--LISCRRE	290
Db	443	GTCTALFSPVPVIYVWSVFL---RCVKYVFPFSPKPPSSVDEYFSDQPLRNLLLSTSEE	498
Qy	291	EVDAC-----ATAVMSPEE	304
Db	499	QTERCFPIENASIIITEIEE	517
RESULT 6			
A32694			
interferon alpha/beta receptor precursor - human			
C:Species: Homo sapiens (man)			
C>Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004			
A:Accession: A32694; S17112			
R:Uze, G.; Lutfalla, G.; Gresser, I.			
Cell 60, 225-234, 1990			
A>Title: Genetic transfer of a functional human interferon alpha receptor into mouse cell			
A:Reference number: A32694; MUID:90124632; PMID:2153461			
A:Accession: A32694			
A:Molecule type: mRNA			
A:Residues: 1-557 <UZE>			
A:Cross-references: UNIPROT:P17181; UNIPARC:UPI000002D51B; GB:J03171; NID:G184645; PIDN:1			
R:Lutfalla, G.			
submitted to the EMBL Data Library, July 1991			
A:Description: The structure of the human interferon alpha/beta receptor gene.			
A:Reference number: S17112			
A:Accession: S17112			
A:Molecule type: DNA			
A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>			
A:Cross-references: UNIPARC:UPI0000179801; EMBL:X60459; NID:G32671			
C:Genetics:			
A:Gene: GDB:IFNARI; IFNAR; IFRC			
A:Cross-references: GDB:120078; OMIM:107450			
A:Map position: 21q22.1-21q22.1			
A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3			
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein			
F:1-21/Domain: transmembrane #status predicted <TRN1>			
F:437-455/Domain: transmembrane #status predicted <TRN2>			
F:50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate (Asp			
Query Match 10.6%; Score 173.5; DB 2; Length 557;			
Best Local Similarity 22.3%; Pred. No. 2.6e-07;			
Matches 72; Conservative 55; Mismatches 113; Indels 83; Gaps 17;			
Qy	21	YALIPCLLTDEVAIIAPQNLSVLSTNNKHLIIMWSVPVIAAGTIVYYSVYQGEYESLYT-	79
Db	215	YSPVHCIKTTVENELPPENIEVSQONQYVLKW-----DYTYANMTFQVWLHAFLK	267
Qy	80	----SHIWPSSWCSLTEGPECVDTDITATVPYN-----LRVRATLGSOTSAMS--	125
Db	268	RNPGNHLY---KWQI---PDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSPWSEE	321
Qy	126	-----ILKHFPNRRNSITLTPGMETIKDGFHLVI-----ELEDLGPQFEF	165
Db	322	IKFDTEIQAFLLPPVFNIRS-----LSDSFHIVIGAPKQSGNTPVIQDPLIYE-	370
Qy	166	LVATVWRPEPGAEEHVWVRSGGIPVHLETMEPGAAYCVKAQ--TFVKAIGRYSAFSQTEC	223
Db	371	-IIFWENTSNAERKIIIEKT---DYTVNPLKPLTVYCVKARAHTMDEKLKSSVFSDAVC	426

```
QY 224 VEQV-GEAIPVLVLFVGMFLILVVVFLFVWMKGRLLQYSCCPVVVLPDLTKITNS-- 280
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 427 EKTGNTSKWL-----IVGICIALPALPFIYAAKVFLR--CINVVFP-SLKPSSID 479
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 -----PQK--LLSCREEVDAC 295
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 480 EYFSEQFLKLLSLTSEEQIEK 502
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
A49947
Interferon gamma receptor beta subunit - mouse
N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type I
C:Species: Mus musculus (house mouse)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49947
R:Hemmi, S.; Bonni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A:Title: A novel member of the interferon receptor family complements functionality of
A:Reference number: A49947; MUID:94170381; PMID:8124717
A:Accession: A49947
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-332 <HEM>
A:Cross-references: UNIPROT:Q63953; UNIPARC:UPI0000022068; GB:S69336; NID:G545841; PIDN:
A:Experimental source: early B-cell line Y16
A>Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
C:Keywords: cytokine receptor

Query Match          9.9%; Score 163; DB 2; Length 332;
Best Local Similarity 27.3%; Pred. No. 1.2e-06;
Matches 73; Conservative 34; Mismatches 100; Indels 60; Gaps 17;

QY 17 MNEFFALICLL-----TDEVAIPAPQNLVSLTNMKHLLMSPVIAGETVY 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 LW-----LPSLLCGLGAASPDSPSQAALPNPLHLNDEQILTWEF--SPSSNDPR 58
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 SVEYQGEVSLYTSHIWIPSSWCSLSTEGPEC-DVTD---DITA-----TVPYN--LRV 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 PVYQVEYS-----FDGSHWRLLE-PNCTDIETKCDLGGRLKLPHPFTVFLRV 110
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 RATLQSTSAWSILKHPFNRSNTILTRP--GMEITKDGPHLVIELE---DL--GPQFEPL 166
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 RAKRGNLTSKWGLE-PFOHYENVTVGPPKNSIVTPGKSLVTHFSPPDPVHGATFQYL 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 VAYWRPQAEHVK-MVRSIGPIVILETMEPGAAVCVKAQTFV-----KAIGRYSAFSQT 221
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 VHYWEKSETQOEQVEGPFKSNISIV--LGNLKPVRVYCLQTEAQLILKNKKIRPHGLLSNV 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 ECVEVQGEA-----IPLVLALFAPV 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 SCHETTANASARLQVILLPLGIFALL 254
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
I56215
Interleukin-10 receptor - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56215
R:Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.
J. Immunol. 152, 1821-1829, 1994
A:Title: Expression cloning and characterization of a human IL-10 receptor.
A:Reference number: I56215; MUID:194165477; PMID:8120391
A:Accession: I56215
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-578 <RES>
A:Cross-references: UNIPROT:Q13651; UNIPARC:UPI00000012BB; EMBL:U00672; NID:G482802; PID
C:Genetics:
A:Gene: GDB:IL10R; HIL-10R
A:Cross-references: GDB:330958; OMIM:146933
```

```
A:Map position: 11q23.3-11q23.3
C:Superfamily: interleukin-10 receptor IL10R
C:Keywords: cytokine receptor

Query Match          9.0%; Score 148; DB 2; Length 578;
Best Local Similarity 22.7%; Pred. No. 4.9e-05;
Matches 68; Conservative 46; Mismatches 107; Indels 78; Gaps 12;

QY 23 LIPCLLTDEVAJ-----LPAPQNLVSLTNMKHLLMSPVIAGETVYYSVE 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MLPCLVLLAALLSLRGLSDAHGTLPSPSPVWFAEFPHHILHWTFIPNQSESTCYEVA 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 YQGEVSLYTSHIWIPSSWCSLSTEGPEC-DVTDITATVPYNLRVRATIGSOTSASILK 128
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 L-----LRYGIESMNSISNCSQTLSDYLTAVTLDLVHNSGYRVRVAVDGRSHSNWTVTN 115
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 HPFNRSNTILT-----RPGMEITKDGPHLVIELEDLGPQF-EFLV 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 TRFSVDEVTLTVGSVNLEIHNGFILGKIQLPRKMAPANDTY-----ESIFSHFREYEI 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 168 AYWRREPG-----AEEHVKVRSRGGIPVHLETMEBPGAAVCVKAQTFVKAIGRYSAP 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 AI-RKVPGNFTTHKKVKHENSFLTSGEV-----GEFCVQVKSVAASRNSKGMW 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 219 SQTCEVEV--QGEAIPVLVLFVFMFLILVVVFLFVWMKGRLLQYSCCPVVVL 271
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 SKEECISLTRQVTVTNVIIPFAFVLLLSGALAYCLALQLYVRRKKL-----PSVLL 271
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
KFRB3
Tissue factor precursor - rabbit
N:Alternate names: coagulation factor III
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JU0441; S23681
R:Andrews, B.S.; Rehentulla, A.; Fowler, B.J.; Edgington, T.S.; Mackman, N.
Gene 98, 265-269, 1991
A:Title: Conservation of tissue factor primary sequence among three mammalian species.
A:Reference number: JU0441; MUID:91200676; PMID:1840552
A:Accession: JU0441
A:Molecule type: mRNA
A:Residues: 1-232 <AND>
A:Cross-references: UNIPROT:P24055; UNIPARC:UPI0000136CA5; GB:M55390; NID:G165696; PIDN:
A:Experimental source: brain
R:Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.
Thromb. Haemost. 66, 315-320, 1991
A:Title: Molecular cloning, characterization and expression of cDNA for rabbit brain tis
A:Reference number: S23681; MUID:92081032; PMID:1746002
A:Accession: S23681
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 33-292 <PAW>
A:Cross-references: UNIPARC:UPI000016CS44; EMBL:X53521; NID:G1495; PIDN:CAA37597.1; PID:
C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor f
C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C:Superfamily: tissue factor
C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F1-32/Domain: signal sequence #status predicted <SIG>
F33-292/Product: tissue factor #status predicted <MAT>
F33-249/Domain: extracellular #status predicted <EXT>
F250-271/Domain: transmembrane #status predicted <EXT>
F272-292/Domain: intracellular #status predicted <INT>
F41.114,154,167,182/Binding site: carbohydrate (Asn) (covalent) #status predicted
F79-87,216-239/Disulfide bonds: #status predicted
F274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match          8.5%; Score 139; DB 1; Length 292;
Best Local Similarity 24.8%; Pred. No. 0.00013;
Matches 63; Conservative 34; Mismatches 99; Indels 58; Gaps 11;

QY 40 NLSVLSTNMKHLMMSPVIAGETVYYSVEYQGEYESTSHI-----WIPSSWCSLST 93
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```



```
Db 63 ---QYGNSTWNDIHCRAQALSCDLTFTTLDLYHRSYGYRVRVRAVDNSQXSNWTTTET 119
QY 130 PNRNSTILT-----RPGWEITKQGFHLVIELEDLGPQFELVAY 169
Db 120 RFTVDEVILTVDSTVKAMDGIYGTIHPRPRTTTPAGDEYEQV--FKDL-RVYKISIRK 176
QY 170 WRREPAAEHHVKM-VRSGGIPVHLEMTPEGAAVCVKQAOTFVKAIGRYSAFSQTCEVEVOG 228
Db 177 FSELKNATKRVKQETFTLTVPIGVR-----KFCVKVLPRLESRIKAEWSEEOCLLIIT 230
QY 229 EAI-----PLVALFAFVGFMILLVVPVLFVKMGRLLOYSCCPVVVL----- 271
Db 231 EQYFTVTNLISILVISMLLFCG-ILVCLVLQWYIRHPGKL-----PTVLVFRKPHDPFPA 283
QY 272 -----PDTLKITT 279
Db 284 NPLCPETPDIAHVD 298

RESULT 12
KFW53
tissue factor precursor - mouse
N;Alternate names: coagulation factor III
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A32318; A39046
R;Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
Mol. Cell. Biol. 9, 2567-2573, 1989
A;Title: A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a protein ho
A;Reference number: A32318; MUID:89343974; PMID:2761539
A;Accession: A32318
A;Molecule type: mRNA
A;Residues: 1-294 <RAN>
A;Cross-references: UNIPROT:P20352; UNIPARC:UPI0000002DD1; GB:M26071; NID:g201924; PIDN:
R;Ranganathan, G.; Blatti, S.P.; Subramaniam, M.; Fias, D.N.; Maible, N.J.; Getz, M.J.
J. Biol. Chem. 266, 496-501, 1991
A;Title: Cloning of murine tissue factor and regulation of gene expression by transformati
A;Reference number: A39046; MUID:91093171; PMID:1985911
A;Accession: A39046
A;Molecule type: mRNA
A;Residues: 1-25, 'I', 27-294 <RAN>
A;Cross-references: UNIPARC:UPI0000001961; GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63
A;Note: 26-Thr was also found
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: Blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-294/Product: tissue factor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;252-274/Domain: transmembrane #status predicted <TMW>
F;37,57,169,200/Binding site: carboxylate (Asn) (covalent) #status predicted
F;75-83,218-241/Disulfide bonds: #status predicted
F;275/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 7.7%; Score 126.5; DB 1; Length 294;
Best Local Similarity 23.7%; Pred. No. 0.0017;
Matches 75; Conservative 41; Mismatches 113; Indels 87; Gaps 17;

QY 22 ALIP-----CLLTDEVAAILPAQ---NLSVLSTNMKHLWMSPVIAPGETVY-YSVEYQGE 73
Db 12 ALAPTFLGCLLLQVTAGAGIPEKAFNLTWISTDFKILEWQ----PKPTNYTVTVQISDR 67
QY 74 YESLYTSHWIWPSWCSLTGEGPCDVTDDIT--ATVPYNLRVRATL-----GSQ---- 120
Db 68 -----SRNW--KNKCFSTTDCDITDEIVKDVWTWAYEAKVLSVPRRNSVHGDGDQLVI 119
QY 121 -----TSAWSLTKHPFNERNSTILTRPGM-EITKDGHLVIELED----- 158
Db 120 HGEPPFTNAPKFLPY-----RDTNLQCPVIQQEQGRKLNVVVKOSLFLVRKNGTFFLTL 175
QY 159 ---LGPQFELVAYWR-RBFGAEHHVKMVRSGGIPVHLEMTPEGAAVC--VKAQTFVKAI 212
```

```
Db 176 RQVFGKDLGYIITRYKSGSTGKTKTNTITNFEFSIDV-----BEGVSYCFVQAMIFSRKT 230
QY 213 GRYSAFSQTCEVE---VOGEALPLVLALFAFVGFMILLVVPVLFVKMGRLLOYSCCPV 268
Db 231 NONSPGSSSTVCTEQWKSFLGETLIIIVGAVLLATIFILLISLCKRKNRAGQ----- 284
QY 269 VVLPDPTLKITNSPOKL 284
Db 285 -----KGKNTPSRL 293

RESULT 13
A31555
interferon gamma receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: A31555
R;Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280, 1988
A;Title: Molecular cloning and expression of the human interferon-gamma receptor.
A;Reference number: A31555; MUID:89003065; PMID:2971451
A;Accession: A31555
A;Molecule type: mRNA
A;Residues: 1-489 <AGU>
A;Cross-references: UNIPROT:P15260; UNIPARC:UPI0000002CE40; GB:J03143; NID:g184650; PIDN:
C;Genetic:
A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein

Query Match 7.4%; Score 122; DB 2; Length 489;
Best Local Similarity 21.2%; Pred. No. 0.0079;
Matches 60; Conservative 54; Mismatches 103; Indels 66; Gaps 12;

QY 35 LPAPQNLSQLSTNMKHLWMSPVIAPGETVY-----YSVEYQGEYSLYTSHWIPSSW 88
Db 29 VFTPTNTIETSYNMPPIVYWEYQIMPEQVPFVTKVYGVK-----NSEWIDA-- 76
QY 89 CSLTEGPECDVTDITATVPYN---LRVRATLGSQTSAMSLKHPNRRNSTILTRPGMEI 145
Db 77 CINISHHYCNISDHVGD--PSNSLWVRVKARVGKESAYAKGEFAVCRDGIKIGPKLDI 134
QY 146 TKDGFHLVIEL-----EDLGPQFELVAYWR---REPGAEEHVKMVRSG--- 186
Db 135 RKEEQKIMIDIFHPSVFVNGDQEVYDPTTCYIRVYVYVMNGSEIQYKILTQKEDD 194
QY 187 -----GIPVHLEMTPEGAAVCVKQAOTFVKAIGRYSAFSQTCEVEVQGEA-----IP 232
Db 195 CDEIQCOLAIPV-----SSLNSQYCVSAEGLVHWGVTTTEKSEKVCITIFNSSIKGSLWIP 250
QY 233 LVLALFAFVGFMILLVVPVLFVKMGRLLOYSCCPVVVLPTL 275
Db 251 VVAALLLFL--VLSLVFICFYIKINPLKES-----IILPKSL 287

RESULT 14
KFB03
tissue factor precursor - bovine
N;Alternate names: coagulation factor III
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1319
R;Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A;Title: cDNA and amino acid sequences of bovine tissue factor.
A;Reference number: JQ1319; MUID:92109720; PMID:1764065
A;Accession: JQ1319
A;Molecule type: mRNA
A;Residues: 1-292 <TAK>
A;Cross-references: UNIPROT:P30931; UNIPARC:UPI0000136CA3; GB:S74147; NID:g241438; PIDN:
A;Experimental source: adrenal gland
```

A;Note: part of this sequence, including the amino end of the mature protein, was confirmed  
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor  
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain  
C;Superfamily: tissue factor  
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane  
F;1-35/Domain: signal sequence #status predicted <SIG>  
F;16-292/Product: tissue factor #status experimental <MAT>  
F;36-248/Domain: extracellular #status predicted <EXT>  
F;249-271/Domain: transmembrane #status predicted <TM>  
F;272-292/Domain: intracellular #status predicted <INT>  
F;43,153,181/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;81-89,215-238/Disulfide bonds: #status predicted  
F;118,124/Binding site: carbohydrate (Thr) (covalent) #status predicted  
F;274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 7.1%; Score 117.5; DB 1; Length 292;  
Best Local Similarity 19.8%; Pred. No. 0.01;  
Matches 49; Conservative 41; Mismatches 101; Indels 57; Gaps 9;

QY 40 NLSVLTNNMKHLMWSPVAPGTVVYSVEYQGEYSLYTSHI-----WIPSSWCSLITE 93  
DB 43 NITKSTNFKTILEWEP-----KPINHVYTVQISPRLGNW--KPKCFYTT 85  
QY 94 GPCEVDVDDITATVPYNLRVRATLGSQTSAMSIKHPFNRR-----STILTRPGME-I 145  
DB 86 NTECDVTDELVKNNRTEYLARVLSYPADTSSSVPEPTNSPFTPYLETNLQPTIQSF 145  
QY 146 TKDGFHLVIELED-----LGPQFEFLVAYRRPFGAEHVNRVSSGGI 188  
DB 146 EQVGTGLNVTVDARTLVANSAPLSLRDVGKDLNVTLYWKASSTGKKKATNTNG-- 203  
QY 189 PVHLETMEPGAACVKAQTFV--KATGRYSAFQTECVQGEAIPLVLFALFAFVGFMIL 246  
DB 204 --FLIDVDKGENYCFHVQAVILSRVNRNQSPEPIKTSHEK---VLSTELFPIIGTVML 258  
QY 247 LVVVPLFV 254  
DB 259 VIIIFIVW 266

RESULT 15  
A32385  
erythropoietin receptor precursor, membrane-bound form - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Sep-1990 #sequence revision 05-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: A41686; A32385; S13249  
R;Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.  
Mol. Cell. Biol. 11: 5527-5533, 1991  
A;Title: Unregulated expression of the erythropoietin receptor gene caused by insertion  
A;Reference number: A41686; MUID:92017832; PMID:1656233  
A;Accession: A41686  
A;Molecule type: mRNA  
A;Residues: 1-507 <HIN>  
A;Cross-references: UNIPROT:P14753; UNIPARC:UPI000000B997; GB:S59388; NID:g237036; PIDN:  
R;D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.  
Cell 57, 277-285, 1989  
A;Title: Expression cloning of the murine erythropoietin receptor.  
A;Reference number: A32385; MUID:89195238; PMID:2539263  
A;Accession: A32385  
A;Molecule type: mRNA  
A;Residues: 1-507 <DAA>  
A;Cross-references: UNIPARC:UPI000000B997; GB:J04843; NID:g193090; PIDN:AAA37571.1; PID:  
A;Experimental source: murine erythroleukemia (MEL) cells, subclone 745  
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
J. Mol. Biol. 216, 567-575, 1990  
A;Title: Characterization of murine erythropoietin receptor genes.  
A;Reference number: S13249; MUID:91080149; PMID:2175360  
A;Accession: S13249  
A;Molecule type: DNA; mRNA  
A;Residues: 1-507 <KUR>  
A;Cross-references: UNIPARC:UPI000000B997; EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:  
A;Experimental source: murine erythroleukemia K-1 cells

C;Genetics:  
A;Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3  
C;Superfamily: erythropoietin receptor; cytokine receptor homology  
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-249/Product: erythropoietin receptor #status predicted <MAT>  
F;25-249/Domain: extracellular #status predicted <EXT>  
F;52-238/Domain: cytokine receptor homology <CRS>  
F;250-271/Domain: transmembrane #status predicted <TM>  
F;272-507/Domain: intracellular #status predicted <INT>  
F;52-62,90-106/Disulfide bonds: #status predicted  
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.8%; Score 111; DB 1; Length 507;  
Best Local Similarity 22.5%; Pred. No. 0.077;  
Matches 71; Conservative 41; Mismatches 97; Indels 106; Gaps 18;

QY 26 CLITDTSVAIIPAP-----QNLSVLTNNMKHLL-MNSPVIAPGETVY 65  
DB 16 CULLAGAAWAPSPSLPDPKFESKAALLASRGSEELICFTORLEDLVCFWEENASSGMDFN 75  
QY 66 YSVEYQGEYSLYTSHIWPSSWCSLITEGPE-----CDV-TDDITATVPYNLRVRAT 116  
DB 76 YSFSYQLEGESRRKS-----CSLHQAPTVRGSRVFWCSLPTADTSSFVPLELQVTEA 126  
QY 117 LGSQTSAMSIKHPFNRR-----NSTILTRPGMEI-----TKDGFHLVIELEDLGPQFEFLVA 168  
DB 127 SGSPR-----YHRIITHINEVLLDAPAGLLARRABEGSHVLR----- 164  
QY 169 YNRREPGA--EEHVKNV-----RSGGIPVHLETMEPGAAYCVKAQ-----TF-VKA 211  
DB 165 -WLPPEGAPMTTHIRVEVDVSAGNRAGGTQ-RVEVLE-GRTECVLSNLRGGTRYTAVRA 221  
QY 212 -----IGRYSAFQTECVQGEAIPLVLFALFAFVGFMILVIVVPLFVWKMG-----R 259  
DB 222 RMAEPSFGFSWASWSEPASILLTASDLDPILLTL-----SLILVLSILLTLVALLSHRR 275  
QY 260 LLOYSCCPVVVLPDT 274  
DB 276 TLQQKIWPFGIPSPES 290

Search completed: April 5, 2006, 11:41:47  
Job time : 20.3576 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:30:18 ; Search time 110.866 Seconds

(without alignments)

1979.144 Million cell updates/sec

Title: US-09-745-792A-14

Perfect score: 1644

Sequence: 1 MQFTFWLSEIWTSLFWFF.....VDCATAVMSPEELLRAWIS 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1644	100.0	311	1 I20RB_HUMAN	O6uxl0 homo sapien
2	712	43.3	147	2 Q8IYV5_HUMAN	Q8IYV5 homo sapien
3	265.5	16.1	230	2 Q4TB36_TETNG	Q4TB36 tetraodon n
4	209	12.7	569	2 Q9YHW0_CHICK	Q9YHW0 gallus gall
5	208	12.7	569	2 Q5XPI1_CHICK	Q5XPI1 gallus gall
6	204	12.4	325	1 I10R2_HUMAN	Q08334 homo sapien
7	199.5	12.1	334	2 Q5RL90_CHICK	Q5RL90 gallus gall
8	195.5	11.9	327	2 Q6ZVU9_HUMAN	Q6ZVU9 homo sapien
9	189.5	11.5	590	1 INAR1_MOUSE	F33896 mus musculus
10	188.5	11.5	337	1 INGR2_HUMAN	F38484 homo sapien
11	185.5	11.3	590	2 Q8OU88_MOUSE	Q8OU88 mus musculus
12	183.5	11.2	590	2 Q8OUJ3_MOUSE	Q8OUJ3 mus musculus
13	182	11.1	449	2 Q5XV05_CHICK	Q5XV05 gallus gall
14	181.5	11.0	349	1 I10R2_MOUSE	Q61190 mus musculus
15	181.5	11.0	560	1 INAR1_BOVIN	Q04790 bos taurus
16	179	10.9	351	2 Q8VHM7_MOUSE	Q8VHM7 mus musculus
17	178.5	10.9	442	2 Q9PVJ9_CHICK	Q9PVJ9 gallus gall
18	176.5	10.7	477	2 Q4R727_MACFA	Q4R727 macaca fasc
19	175.5	10.7	341	2 Q9YGC8_CHICK	Q9YGC8 gallus gall
20	173.5	10.6	557	1 INAR1_HUMAN	F17181 homo sapien
21	173.5	10.6	557	2 Q53H11_HUMAN	Q53H11 homo sapien
22	173.5	10.6	560	1 INAR1_SHEEP	Q28589 ovis aries
23	172.5	10.5	557	2 Q53GW9_HUMAN	Q53GW9 homo sapien
24	165.5	10.1	305	2 Q6DCU5_XENLA	Q6DCU5 xenopus lae
25	165	10.0	435	2 Q7ZT26_TETNG	Q7ZT26 tetraodon n
26	163.5	9.9	333	2 Q7ZT30_TETNG	Q7ZT30 tetraodon n
27	163.5	9.9	546	1 I20RA_MOUSE	Q6phb0 mus musculus
28	163	9.9	332	2 Q78EC1_9MURI	Q78EC1 mus sp. int
29	163	9.9	332	2 Q63953_MOUSE	Q63953 mus musculus
30	160.5	9.8	508	2 Q6QIU4_CHICK	Q6QIU4 gallus gall
31	160.5	9.8	569	2 Q99ND6_RAT	Q99ND6 rattus norv

32	158.5	9.6	508	2 Q9PVK0_CHICK	Q9PVK0 gallus gall
33	155.5	9.5	362	2 Q764M7_PIG	Q764M7 sus scrofa
34	155.5	9.5	508	2 Q9YHV9_CHICK	Q9YHV9 gallus gall
35	155	9.4	553	1 I20RA_HUMAN	Q9uhf4 homo sapien
36	154.5	9.4	301	2 Q7ZT35_TETNG	Q7ZT35 tetraodon n
37	154.5	9.4	338	2 Q800G2_TETNG	Q800G2 tetraodon n
38	153.5	9.3	317	2 Q58CP3_BOVIN	Q58CP3 bos taurus
39	153	9.3	560	1 INAR1_PIG	Q764m8 sus scrofa
40	151.5	9.2	263	1 I22RA_HUMAN	Q969f5 homo sapien
41	151	9.2	345	2 Q4TIA7_TETNG	Q4TIA7 tetraodon n
42	149.5	9.1	213	2 Q8C352_MOUSE	Q8C352 mus musculus
43	148.5	9.0	336	2 Q800E8_TETNG	Q800E8 tetraodon n
44	148	9.0	578	1 I10R1_HUMAN	Q13651 homo sapien
45	140.5	8.5	520	1 I28RA_HUMAN	Q8Iu57 h interleuk

#### ALIGNMENTS

##### RESULT 1

ID	I20RB_HUMAN	STANDARD;	PRT;	311 AA.
AC	Q6UXL0; Q6P438; Q8TAJ7;			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Interleukin-20 receptor beta chain precursor (IL-20R-beta) (IL-20R2).			
GN	Name=IL20RB; Synonyms=DIRS1; ORFNames=UNQ557/PRO1114;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).			
RX	MEDLINE=22987296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,			
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,			
RA	Wood W.I., Godowski P.J., Gray A.M.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
RL	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).			
RP	TISSUE=Cervix, and Skin;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan T., Moore T., Max S.I., Wang J., Heien F.,			
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,			
RA	Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

[3] PROTEIN SEQUENCE OF 30-44 (ISOFORM 1).  
 RP PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RL verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824(2004).  
 [4]  
 RP SUBUNIT, LIGAND-BINDING, AND TISSUE SPECIFICITY.  
 RX MEDLINE=21097717; PubMed=11163326; DOI=10.1016/S0092-8674(01)00187-8;  
 RA Blumberg H., Conklin D., Xu W.F., Grossmann A., Brendler T.,  
 RA Carollo S., Egan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,  
 RA Jellinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,  
 RA Prunkard D., Sexson S., Sprecher C., Waggle K., West J.,  
 RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A.;  
 RT "Interleukin 20: discovery, receptor identification, and role in  
 RL epidermal function.";  
 RL Cell 104:9-19(2001).  
 [5]  
 RP SUBUNIT, AND LIGAND-BINDING.  
 RX PubMed=11564763;  
 RA Dumoutier L., Leemans C., Lejeune D., Kotenko S.V., Renauld J.-C.;  
 RT "STAT activation by IL-19, IL-20 and mda-7 through IL-20 receptor  
 RL complexes of two types.";  
 RL J. Immunol. 167:3545-3549(2001).  
 [6]  
 RP SUBUNIT, AND LIGAND-BINDING.  
 RX PubMed=12351624; DOI=10.1074/jbc.M205114200;  
 RA Parrish-Novak J., Xu W., Brendler T., Yao L., Jones C., West J.,  
 RA Brandt C., Jellinek L., Madden K., McKernan P.A., Foster D.C.,  
 RA Jaspers S., Chandrasekhar Y.A.;  
 RT "Interleukins 19, 20, and 24 signal through two distinct receptor  
 RL complexes: Differences in receptor-ligand interactions mediate unique  
 RT biological functions.";  
 RL J. Biol. Chem. 277:47517-47523(2002).  
 [7]  
 RP SUBUNIT, AND LIGAND-BINDING.  
 RX PubMed=14580208; DOI=10.1021/bi0354583;  
 RA Plotnev S., Magracheva E., Kozlov S., Tobin G., Kotenko S.V.,  
 RA Wlodawer A., Zdanov A.;  
 RT "Characterization of the recombinant extracellular domains of human  
 RL interleukin-20 receptors and their complexes with interleukin-19 and  
 RL interleukin-20.";  
 RL Biochemistry 42:12617-12624(2003).  
 CC -!- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20 and  
 CC IL24. The IL22RA1/IL20RB dimer is a receptor for IL20 and IL24.  
 CC -!- SUBUNIT: Heterodimer with IL20RA and heterodimer with IL22RA1.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q6UXL0-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q6UXL0-2; Sequence=VSP 011499, VSP 011500;  
 CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in skin  
 CC and testis. Highly expressed in psoriatic skin.  
 CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.  
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.  
 CC -----  
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AY358305; AAQ08672.1; -; mRNA.  
 CC EMBL; BC027449; AAH27449.1; -; mRNA.  
 CC EMBL; BC063696; AAH63696.1; -; mRNA.  
 CC Ensembl; ENSG00000174564; Homo sapiens.  
 CC HGNC; HGNC:6004; IL20RB.  
 CC MIM; 605621; -;  
 CC InterPro; IPR000282; Cytok receptor\_2.  
 CC InterPro; IPR003961; FN\_III.

DR Pfam; PF00041; fn3; 1.  
 DR PROSITE; PS0853; FN3; 1.  
 KW Alternative splicing; Direct protein sequencing; Glycoprotein;  
 KW Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 29  
 FT CHAIN 30 311 Interleukin-20 receptor beta chain.  
 FT TOPO DOM 30 233 Extracellular (Potential).  
 FT TRANSMEM 234 254 Potential.  
 FT TOPO DOM 255 311 Cytoplasmic (Potential).  
 FT DOMAIN 36 137 Fibronectin type-III 1.  
 FT DOMAIN 144 228 Fibronectin type-III 2.  
 FT CARBOHYD 40 40 N-linked (GlcNAc . .) (Potential).  
 FT CARBOHYD 134 134 N-linked (GlcNAc . .) (Potential).  
 FT DISULFID 202 223 By similarity.  
 FT VARSPLIC 1 47 Missing (in isoform 2 and isoform 3).  
 FT VARSPLIC 48 142 /FTID=VSP 011499.  
 FT VARSPLIC 48 142 Missing (in isoform 2).  
 FT /FTID=VSP 011500.  
 SQ SEQUENCE 311 AA; 35076 MW; FF366D518116D9E3 CRC64;  
 Query Match 100.0%; Score 1644; DB 1; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-136; Indels 0; Gaps 0;  
 Matches 311; Conservative 0; Mismatches 0;  
 QY 1 MQTFTWVLEEIMTSLFMWFFFYALIPCLLTDEVAIIIPAPQNLVSLSTNMKHLMWSPVIAP 60  
 DB 1 MQTFTWVLEEIMTSLFMWFFFYALIPCLLTDEVAIIIPAPQNLVSLSTNMKHLMWSPVIAP 60  
 QY 61 GETVYSVEYQGEYSLSYTHSWISSCSLSTEGPECVDVTDITATVPYNLRVATLGSQ 120  
 DB 61 GETVYSVEYQGEYSLSYTHSWISSCSLSTEGPECVDVTDITATVPYNLRVATLGSQ 120  
 QY 121 TSAMSLIKHPFNRSITLTPGWEITKGFHVLIELELGPQFELVAYWRREPGEAEHV 180  
 DB 121 TSAMSLIKHPFNRSITLTPGWEITKGFHVLIELELGPQFELVAYWRREPGEAEHV 180  
 QY 181 KMRVSGGIPVHLEMTPEGAAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240  
 DB 181 KMRVSGGIPVHLEMTPEGAAAYCVKAQTFVKAIGRYSAFSQTCEVQGEAIPLVLALFAP 240  
 QY 241 VGFMLILVVPLFVWVGRLQYSCCPVVLDPDTKITNSPKLISCRREEVDACATVM 300  
 DB 241 VGFMLILVVPLFVWVGRLQYSCCPVVLDPDTKITNSPKLISCRREEVDACATVM 300  
 QY 301 SPEELLRAWIS 311  
 DB 301 SPEELLRAWIS 311  
 RESULT 2  
 Q8IYI5 HUMAN  
 ID Q8IYI5\_HUMAN PRELIMINARY; PRT; 147 AA.  
 AC Q8IYI5;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE FNDG6 protein.  
 GN Name=FNDG6;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skin;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Hopkins R.F., Jordan H., Moore K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.B., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Skin;  
RG NIH MGC Project;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
DR EMBL; BC033292; AAH33292.1; -; mRNA.  
DR Ensembl; ENSG00000174564; Homo sapiens.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR InterPro; IPR000282; Cyto\_k\_receptor\_2.  
KW Receptor; Transmembrane.  
SQ SEQUENCE 147 AA; 16945 MW; 71BAP49274618999 CRC64;

Query Match 43.3%; Score 712; DB 2; Length 147;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MKHLLMWSPIAPGETVYVSVEQGEYSLETHSHIIPSWCSLTGPGPCDVTDDITATV 107  
DB 1 MKHLLMWSPIAPGETVYVSVEQGEYSLETHSHIIPSWCSLTGPGPCDVTDDITATV 60  
QY 108 PYNLRVRATIGSOTSAWSILKHPNENSTLTTPGMEITKDGPHLVIELEDLGPQFEFLV 167  
DB 61 PYNLRVRATIGSOTSAWSILKHPNENSTLTTPGMEITKDGPHLVIELEDLGPQFEFLV 120  
QY 168 AYWRREPGEAE 178  
DB 121 AYWRREPGEAE 131

RESULT 3  
Q4TB36\_TETNG PRELIMINARY; PRT; 230 AA.  
AC Q4TB36;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Chromosome undetermined SCAP7209, whole genome shotgun sequence.  
GN ORFNames=GSTENG0000391001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorphia; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontoidea; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Nautilon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Blomont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAEA01007209; CAF89896.1; -; Genomic\_DNA.  
DR InterPro; IPR000282; Cyto\_k\_receptor\_2.  
DR InterPro; IPR0003961; FN\_III.  
DR PROSITE; PS50853; FN3; 1.  
KW Repeat; Transmembrane.  
SQ SEQUENCE 230 AA; 25422 MW; 4483631CFC3807D1 CRC64;

Query Match 16.1%; Score 265.5; DB 2; Length 230;  
Best Local Similarity 31.8%; Pred. No. 6.4e-15;  
Matches 71; Conservative 35; Mismatches 84; Indels 33; Gaps 6;

QY 23 LIPCLLT-----DEVAILPAPQNLVSLTNMKHLLMWSPIAPGET-VYVSVEQGEY 74  
DB 9 LLPMTTMMKTSQDGV-----APGGPRMDSLNNRHLVLRPLQDNCSTALVYSVQGEF 65  
QY 75 ESLYTSHIWIPSWCSLTGPGPCDVTDDITATVPYNLRVRATIGSOTSAWSILKHPNEN 134  
DB 66 ELSVLNDSWVDAAGCQRTGTGCDLTGDSYDLRLRAHCGAQTSAWSRSSSPFNRR 125  
QY 135 STILTPGMEITKDGPHLVIELEDLGPQFEFLVAYVRR-----EPGA 176  
DB 126 DTVLTAPLMKVASSEGALRVSLSEPRLTLLVVEWVRGEEQATALLPEQTLLVPTL 185  
QY 177 EHVHVMVRSGGIP---VHLETMPGAAYCVKAQTFVKAIGRYS 216  
DB 186 QVGERVLRAGPTPCWEVRNSNGEPHAV-CHPSRSQVWVYKLS 227

RESULT 4  
Q9YHW0\_CHICK PRELIMINARY; PRT; 569 AA.  
AC Q9YHW0;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Interferon alpha/beta receptor 1.  
GN Names=IFNAR1;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=liver;  
RX MEDLINE=99177346; PubMed=10077530;  
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;  
RT "Comparative genomic analysis of the interferon/interleukin-10  
RT receptor gene cluster.";  
RL Genome Res. 9:242-250(1999).  
DR EMBL; AF082664; AAD13669.1; -; mRNA.  
DR Ensembl; ENSGALG0000015942; Gallus gallus.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR000282; Cyto\_k\_receptor\_2.  
DR InterPro; IPR0003961; FN\_III.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS50853; FN3; 4.  
KW Receptor.  
SQ SEQUENCE 569 AA; 64055 MW; 6A757DDFB891E605 CRC64;

Query Match		12.7%; Score 209; DB 2; Length 569;
Best Local Similarity		25.2%; Pred. No. 1.8e-09;
Matches		79; Conservative 52; Mismatches 125; Indels 58; Gaps 14;
QY	21	YALIPCL-LTDEVAIIPAPONLSVLSTNMKHLWSPVAPGETVYVSVEY-OGEYESLY 78
DB	222	FSPHICIKTRKVNLDLCPNTNRVFAFNKFKYLLNDNHY--NSHVITYTVQYLTGYLKNLY 279
QY	79	T--SHWIPSSWCSLTEGPECDDTDDITAT-VPNYLRVRATLGSQTSAWS-----125
DB	280	DYSSKQKVGCGENITSMKNLSSVVKPTASYYFRVQAMNEYSKSLCKDVEVDPVPT 339
QY	126	-----ILKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPQFELVAYWR 171
DB	340	NEIGPPDVKVDISDVLH-----IKITPPG-----GPGNKIMSDLYD-----FSYQILYWK 385
QY	172	REPGBAEHVKNVRSGGIPVHLETMPEGAAYCVKAQTFVKAIGRYSAFSQTECV-EVQGEA 230
DB	386	NSDNEEEVKMKETKTQTIATVSDLPASTLYCVKQVAFSEAYNKSSDFSREECIGTAGGKH 445
QY	231	IPVLALFAFVGMFLILVVVP-----LFVWKGRLLOYSCCPVVVLPDTL-----KITNSP 281
DB	446	LPILII-LATFAGALTVLIVASLIVFLYQVYNKIKYMFPPSCQTPINIEGFGAQLFSSP 504
QY	282	QKLISCRREEVDAC 295
DB	505	--FVPTVEPVEIC 516
RESULT 5		
Q5XP11 CHICK PRELIMINARY; PRT; 569 AA.		
AC	Q5XP11	
DT	25-OCT-2004	(T-EMBLrel. 28, Created)
DT	25-OCT-2004	(T-EMBLrel. 28, Last sequence update)
DT	25-OCT-2004	(T-EMBLrel. 28, Last annotation update)
DE	Interferon receptor.	
GN	Names=IFNARI;	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Liver;	
RA	Han C.-L., Wang M., Gao F., Wu Z.-G.;	
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY741159; AAU93528.1; -; mRNA.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	InterPro; IPR000282; Cytok_receptor_2.	
DR	InterPro; IPR003961; FN_III.	
DR	SMART; SM00060; FN3; 3.	
KW	PROSITE; PS00853; FN3; 4.	
QY	569	AA; AEC99111A5476FBF CRC64;
Query Match		12.7%; Score 208; DB 2; Length 569;
Best Local Similarity		25.2%; Pred. No. 2.1e-09;
Matches		79; Conservative 52; Mismatches 125; Indels 58; Gaps 14;
QY	21	YALIPCL-LTDEVAIIPAPONLSVLSTNMKHLWSPVAPGETVYVSVEY-OGEYESLY 78
DB	222	FSPHICIKTRKVNLDLCPNTNRVFAFNKFKYLLNDNHY--NSHVITYTVQYLTGYLKNLY 279
QY	79	T--SHWIPSSWCSLTEGPECDDTDDITAT-VPNYLRVRATLGSQTSAWS-----125
DB	280	DYSSKQKVGCGENITSMKNLSSVVKPTASYYFRVQAMNEYSKSLCKDVEVDPVPT 339
QY	126	-----ILKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPQFELVAYWR 171
RESULT 6		
I10R2 HUMAN STANDARD; PRT; 325 AA.		
ID	I10R2_HUMAN	
AC	Q08334; Q9BUU4;	
DT	01-FEB-1995	(Rel. 31, Created)
DT	01-FEB-2005	(Rel. 46, Last sequence update)
DT	10-MAY-2005	(Rel. 47, Last annotation update)
DE	Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)	
DE	(Cytokine receptor family 2 member 4) (Cytokine receptor class-II,	
DE	member 4) (CRF2-4).	
GN	Name=IL10RB; Synonyms=CRFB4;	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Fetal brain;	
RX	MEDLINE=93300510; PubMed=8314576;	
RA	Lutfalla G., Gardiner K., Uze G.;	
RT	"A new member of the cytokine receptor gene family maps on chromosome	
RT	21 at less than 35 kb from IFNAR.";	
RL	Genomics 16:366-373 (1993).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RX	MEDLINE=96054036; PubMed=7563119; DOI=10.1007/BF00186545;	
RA	Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;	
RT	"Structure of the human CRFB4 gene: comparison with its IFNAR	
RT	neighbor.";	
RL	J. Mol. Evol. 41:338-344 (1995).	
RN	[3]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	
RA	Kalinine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,	
RA	Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,	
RA	Phelan M., Farmer A.;	
RT	"Cloning of human full-length CDSs in BD Creator(TM) system donor	
RT	vector.";	
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.	
RN	[4]	
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT GLU-47.	
RA	Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,	
RA	Ahearn M.O., Kuldane S.A., Rajkumar N., Toth E.J., Yi Q.,	
RA	Nickerson D.A.;	
RT	"SeattlesNPc. NHLBI HL66682 program for genomic applications, UW-	
RT	FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";	
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.	
RN	[5]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	
RC	TISSUE=Kidney;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,	

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Viallao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP PROTEIN SEQUENCE OF 20-34.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824(2004).  
 RN [7]  
 RP CHARACTERIZATION.  
 RX MEDLINE=97459974; PubMed=9312047; DOI=10.1093/emboj/16.19.5894;  
 RA Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,  
 RA Pestka S.;  
 RT Identification and functional characterization of a second chain of  
 RT the interleukin-10 receptor complex.";  
 RL EMBO J. 16:5894-5903(1997).  
 RN [8]  
 RP CHARACTERIZATION.  
 RX MEDLINE=20469498; PubMed=10875937; DOI=10.1074/jbc.M005304200;  
 RA Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,  
 RA Wood W.I., Goddard A.D., Gurney A.L.;  
 RT Interleukin (IL)-22, a novel human cytokine that signals through the  
 RT interferon receptor-related proteins CRF2-4 and IL-22R.";  
 RL J. Biol. Chem. 275:31335-31339(2000).  
 CC -!- FUNCTION: Receptor for IL10 and IL22. Serves as an accessory chain  
 CC essential for the active IL10 receptor complex and to initiate  
 CC IL10-induced signal transduction events.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.  
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; Z17227; CAA78933.1; -; mRNA.  
 DR EMBL; U08988; AAA86872.1; -; Genomic DNA.  
 DR EMBL; BT009777; AAP88779.1; -; mRNA.  
 DR EMBL; AV323826; AAP72016.1; -; Genomic DNA.  
 DR EMBL; BC001903; A3H01903.1; -; mRNA.  
 DR F1R; A47003; A47003.  
 DR HSSP; P13726; 1TFH.  
 DR ENSEMBL; ENSG00000159113; Homo sapiens.  
 DR HGNC; HGNC:5965; IL10RB.  
 DR H-InvDB; HIX0016074; -.  
 DR MIM; 123889; -; C-integral to membrane; TAS.  
 DR GO; GO:0016021; -; C-integral to membrane; TAS.  
 DR GO; GO:0005886; C:plasma membrane; TAS.  
 DR GO; GO:0004920; F:interleukin-10 receptor activity; TAS.  
 DR GO; GO:0004872; F:receptor activity; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR000282; Cytok receptor 2.  
 DR InterPro; IPR003961; FN III.  
 DR Pfam; PF01108; Tissue fac; I.  
 DR PROSITE; PPS0853; FN3\_FALSE NEG.  
 DR Direct protein sequencing; Glycoprotein; Polymorphism; Receptor;  
 KW Signal; Transmembrane.

FT SIGNAL 1 19 Interleukin-10 receptor beta chain.  
 FT CHAIN 20 325 Extracellular (Potential).  
 FT TOPO\_DOM 20 220 Potential.  
 FT TRANSMEM 221 242 Potential.  
 FT TOPO\_DOM 243 325 Cytoplasmic (Potential).  
 FT DOMAIN 113 205 Fibronectin type-III.  
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 161 161 By similarity.  
 FT DISULFID 66 74 By similarity.  
 FT DISULFID 188 209 K -> E (in dSNP:2834167).  
 FT VARIANT 47 47 /FTID=VAR 020666.  
 FT CONFLICT 124 124 A -> D (in Ref. 2).  
 FT CONFLICT 243 243 A -> S (in Ref. 1 and 2).  
 FT CONFLICT 269 273 FLAGHP -> VGRME (in Ref. 2).  
 FT CONFLICT 274 325 Missing (in Ref. 2).  
 SQ SEQUENCE 325 AA; 36995 MW; E470726619AF54C2 CRC64;  
 Query Match 12.4%; Score 204; DB 1; Length 325;  
 Best Local Similarity 27.1%; Pred. No. 2.5e-09;  
 Matches 79; Conservative 47; Mismatches 113; Indels 52; Gaps 17;  
 QY 12 WTSLFMFPFVAILPCLLTDEVAIPAPONLSVLSTNMKHLMM-SPIVAPGETVYVSVEY 70  
 Db 3 W-SLGSW-----LGGCLLVSAIGALGVPPPNVNVNFKILQWESPAFAKG-----NLTF 52  
 QY 71 QGEYESLTSYHIWIPSSWCSTLGEPCEDVTDITATVPYNLRVRLATLGSGTSAS-SILKH 129  
 Db 53 TAYLSYR-----IFQDKCMNTLTTECDFS-SLSKYGDHTLRVRAEFADEHSDWNITFC 106  
 QY 130 PNRNRSITLITROM--EITKDGPHLVIELEDLGPQE-----FLVAYWR 171  
 Db 107 PV--DDTIIGPGQMQLVLAADSLH-----MRLAPKIENEYETWTMKVNVNWTYNVQYWK 160  
 QY 172 REPGEAEHVKVRSGGIPVHLEMTBPGAAVCVKAQTFVKAIGRYSAFSGTECVVE-VGEA 230  
 Db 161 N--GTDEKFIPTQYDFEV-LRNLEPWYTCVQVRGFLPDRNKAGWSEPVCEQTHDET 217  
 QY 231 IP---LVLAFAFVGFMLILVVVPLF--VWKMGRLLQYSCCPVVVLPDLTK 276  
 Db 218 VFSMVAVILMASV-FMVCLALLGCFALLWCYVVKTKYAFSPRNSLPQHLK 267  
 RESULT 7  
 Q5RL90 CHICK  
 ID Q5RL90 CHICK PRELIMINARY; PRT; 334 AA.  
 AC Q5RL90  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE IFNGR2 (interferon-gamma receptor 2).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Han C.-L., Wang M., Gao F., Wu Z.-G.;  
 RL Submitted (Nov-2004) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Han C.-L., Wang M., Gao F.;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY820753; AAV67776.1; -; mRNA.  
 DR EMBL; AY957508; AAX83125.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain...); IEA.

GO; GO:0007596; P: blood coagulation; IEA.  
 DR InterPro; IPR000282; Cytok\_receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR001187; Tissue\_factor.  
 DR Pfam; PF01108; Tissue\_fac; I.  
 DR PROSITE; PS00853; PN3; 2.  
 DR Receptor.  
 SQ SEQUENCE 334 AA; 37698 MW; 5951976B878FC1F6 CRC64;  
 Query Match 12.1%; Score 199.5; DB 2; Length 334;  
 Best Local Similarity 24.7%; Pred. No. 6.3e-09;  
 Matches 79; Conservative 58; Mismatches 130; Indels 53; Gaps 17;  
 QY 15 LFMWFFYALIPCLL--TDREVAIPAPONLSVLSTNMKHLMLMWSPVIAFGETVYYSVEYQ- 71  
 ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :  
 Db LFLVGIFLLGPAPAPGTEASPHLPAPEDVMVYSFNFCSLRLWSPVKVDGGSVTVQFKT 67  
 QY 72 GEYESIYTHIMIPSW-----CSLREGPCDVTDDITA---TVPNLRVRLATIGSOTSAS 124  
 ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :  
 Db GAP-----NHWSEMDCTRITQTECSFLKSVKERRWTVV--LRVRAEMGRTSAW 114  
 QY 125 SILKHPF--NRNSTI-LTRPGMEITKDGPHLVELEDLGPQ-----FEFLVAYWRREPQAE 177  
 ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :  
 Db 115 -VTDFPVAERNITIGPPKNSVIVSSDLSLISVTTPPGPFGVHLQTHVSIWNTIITT 173  
 QY 178 EHVYKVRSGGIPVHLETFMFGAAYCVKAQTFVKAIGRYSAFS-QT--BCVEV---QGEAI 231  
 ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :  
 Db 174 K--KEIKTSNTLPKIDKLAQSTLYCFTIQIELMTYSRFLHGLQTVPECYRTTISEATKA 231  
 QY 232 PLVLALPAFVGFMILIVVPLF-VNMGRLLOYSCCPVVLP-----DTLKITNSPKQLIS 286  
 ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :  
 Db 232 GYIVAFMSVGLLIIIVIGFFCLRNRKAIKYLSPQLRIPSPHFEEYLRDPSMPQLEVL 291  
 QY 287 CRREEVDACATAMSPPEELL 306  
 ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :  
 Db 292 ENHDE-----DPQDL 302  
 RESULT 8  
 Q6ZVU9 HUMAN  
 ID Q6ZVU9 HUMAN PRELIMINARY; PRT; 327 AA.  
 AC Q6ZVU9;  
 DT 05-JUL-2004 (T:EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T:EMBLrel. 27, Last sequence update)  
 DE 05-JUL-2004 (T:EMBLrel. 27, Last annotation update)  
 DE Hypothetical protein FLJ42063.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Synovial membrane tissue;  
 RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,  
 RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,  
 RA Matsumura Y., Moriya S., Chiba E., Moniyama H., Onogawa S.,  
 RA Kaeriyama S., Satoh N., Matsumura H., Takahashi E., Kataoka R.,  
 RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,  
 RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Saito H., Wakamatsu A.,  
 RA Ighii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,  
 RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,  
 RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,  
 RA Takahashi-Fujii A., Ohshima A., Sugiyama A., Kawakami B., Suzuki Y.,  
 RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 CC -/- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 EMBL; AK124057; BAC85761.1; -; mRNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000282; Cytok\_receptor\_2.  
 KW Receptor; Transmembrane.







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DR GO: GO:0016021; C: integral to membrane; TAS.
DR InterPro: IPR000282; Cytok receptor_2.
DR InterPro: IPR003961; FN_III.
DR SMART: SM00060; FN3; 3.
KW Receptor; Transmembrane.
SQ SEQUENCE 590 AA; 65713 MW; E8383FFA6E3AF3C CRC64;

Query Match 11.2%; Score 185.5; DB 2; Length 590;
Best Local Similarity 23.7%; Pred. No. 3.2e-07;
Matches 80; Conservative 62; Mismatches 153; Indels 43; Gaps 16;

QY 3 TFTWLEETWISLFFMFFFYALIPCLTDEVAIPAPONLSVLSTNMKHLIMSPVIAPGE 62
DB 197 TYCLEVKAHPSLKXHSNSTVQCISTTAVANKMPVPGNLQVDAQGKSYVLKWD-YIASAD 255
QY 63 TVY-----YSVEYQGEYESLYTSHIWPSSWCSLTGEPEDVDITATVPYNLRVRA 115
DB 256 VLFRAQWLPGYSKSSSGS-----RSDKWKPIPTCANVQTHCVFSQDVTVTGTFLLHVQA 310
QY 116 TLGQSOTSAMSLKHPFNRSNTILTRPGMEIT--KDGPHLVIELEDL---GPOFEFLVAYW 170
DB 311 SEGNTHSFWSSEKFDISKHILPPPPVITVAMSDTLVVVNCQDSTCDGLNVE--IIFW 368
QY 171 RREPGEAEHVKMVRSGGIPVHLETMPGAAVCYKAOTFVKA-IGRYSAFSOTECVEVOGE 229
DB 369 --ENTSNTKISMKEKGP-EFTLKNLQPLTVYCVQARVLFALLNKTSNFSEKLCETKTRPG 425
QY 230 APLVLALFAP-VGFMLILVVVPL-FVWKMGRLLQYSCCPVVVLPDLTK--ITNSPOK-- 283
DB 426 SPFTMIITGLGVVFFSVMLYALRSWK---YLCHVCPPLKPPRSIDFFEPSPSKNL 482
QY 284 -LISCR-----EVDACATAVM-SPEELRAWIS 311
DB 483 VLLTAEHTERCPIENTDTVAVEVKHAPEDLRKYSS 520

RESULT 12
ID Q80UJ3_MOUSE PRELIMINARY; PRT; 590 AA.
AC Q80UJ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Ifnar protein (Interferon (Alpha and beta) receptor 1).
GN Names: Ifnar1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; BC043935; AAH43935.1; -; mRNA.
DR EMBL; BC052429; AAH52429.1; -; mRNA.
DR MGI; MGI:107658; Ifnar1.
DR GO: GO:0005615; C: extracellular space; TAS.
DR GO: GO:0016021; C: integral to membrane; TAS.
DR InterPro: IPR000282; Cytok receptor_2.
DR InterPro: IPR003961; FN_III.
DR SMART: SM00060; FN3; 3.
KW Receptor; Transmembrane.
SQ SEQUENCE 590 AA; 65796 MW; E887ADFA6DFEAF3C CRC64;

Query Match 11.2%; Score 183.5; DB 2; Length 590;
Best Local Similarity 23.7%; Pred. No. 3.2e-07;
Matches 80; Conservative 61; Mismatches 154; Indels 43; Gaps 16;

QY 3 TFTWLEETWISLFFMFFFYALIPCLTDEVAIPAPONLSVLSTNMKHLIMSPVIAPGE 62
DB 197 TYCLEVKAHPSLKXHSNSTVQCISTTAVANKMPVPGNLQVDAQGKSYVLKWD-YIASAD 255
QY 63 TVY-----YSVEYQGEYESLYTSHIWPSSWCSLTGEPEDVDITATVPYNLRVRA 115
DB 256 VLFRAQWLPGYSKSSSGS-----RSDKWKPIPTCANVQTHCVFSQDVTVTGTFLLHVQA 310
QY 116 TLGQSOTSAMSLKHPFNRSNTILTRPGMEIT--KDGPHLVIELEDL---GPOFEFLVAYW 170
DB 311 SEGNTHSFWSSEKFDISKHILPPPPVITVAMSDTLVVVNCQDSTCDGLNVE--IIFW 368
QY 171 RREPGEAEHVKMVRSGGIPVHLETMPGAAVCYKAOTFVKA-IGRYSAFSOTECVEVOGE 229
DB 369 --ENTSNTKISMKEKGP-EFTLKNLQPLTVYCVQARVLFALLNKTSNFSEKLCETKTRPG 425
QY 230 APLVLALFAP-VGFMLILVVVPL-FVWKMGRLLQYSCCPVVVLPDLTK--ITNSPOK-- 283
DB 426 SPFTMIITGLGVVFFSVMLYALRSWK---YLCHVCPPLKPPRSIDFFEPSPSKNL 482
QY 284 -LISCR-----EVDACATAVM-SPEELRAWIS 311
DB 483 VLLTAEHTERCPIENTDTVAVEVKHAPEDLRKYSS 520

RESULT 13
ID Q5XY05_CHICK PRELIMINARY; PRT; 449 AA.
AC Q5XY05;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE IFNARI (Fragment)
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Han C.-I., Wang M., Gao F.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723314; AAU85361.1; -; mRNA.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0004896; F: hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro: IPR000282; Cytok_receptor_2.

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determined at the level of receptor (IFNAR) structure.";

RT FEBS Lett. 313:255-259(1992).

RN [2]

RL NUCLEOTIDE SEQUENCE.

RX MEDLINE=93305725; PubMed=8318540; DOI=10.1016/0167-4781(93)90129-2;

RA Lim J.-K., Langer J.A.;

RT "Cloning and characterization of a bovine alpha interferon receptor.";

RL Biochim. Biophys. Acta 1173:314-319(1993).

CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type I IFNs triggers tyrosine phosphorylation of a number of proteins including JAKs, TYK2, STAT proteins and IFN alpha- and beta-subunits themselves.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.

CC -!- SIMILARITY: Contains 3 fibronectin type-III domains.

CC -----

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CC -----

DR EMBL; X68443; CAA48484.1; -; mRNA.

DR EMBL; L06320; AAA02571.1; -; mRNA.

DR PIR; S27387; S27387.

DR InterPro; IPR00282; Cytok receptor\_2.

DR InterPro; IPR003961; FN\_III.

DR InterPro; IPR001187; Tissue factor.

DR Pfam; PF01108; Tissue fac; 1.

DR PROSITE; PS50853; FN3\_2.

KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.

FT SIGNAL 1 24 By similarity.

FT CHAIN 25 560 Interferon-alpha/beta receptor alpha chain.

FT FT

FT TOPO\_DOM 25 437 Extracellular (Potential).

FT TRANSMEM 438 458 Potential.

FT TOPO\_DOM 459 560 Cytoplasmic (Potential).

FT DOMAIN 133 224 Fibronectin type-III 1.

FT DOMAIN 230 326 Fibronectin type-III 2.

FT DOMAIN 334 426 Fibronectin type-III 3.

FT CARBOHYD 47 47 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 55 55 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 85 85 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 109 109 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 172 172 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 254 254 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 313 313 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 377 377 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 434 434 N-linked (GlcNAc..) (Potential).

FT DISULFID 76 84 By similarity.

FT DISULFID 199 220 By similarity.

FT CONFLICT 422 422 F -> V (in Ref. 2).

SQ SEQUENCE 560 AA; 63819 MW; 66D76B72861E1D11 CRC64;

Query Match 11.0%; Score 181.5; DB 1; Length 560;

Best Local Similarity 22.9%; Pred. No. 4.5e-07;

Matches 73; Conservative 62; Mismatches 133; Indels 51; Gaps 14;

QY 21 YALIPCLLTDEVAIPAPONLSVLSTNMKHLMMSPVIAGETVYVYVQGEYESLYTS 80

DB 215 YSPVYCINTERHKVSPENIQINADNQIYVLKW-----DYPENATFQAQWLRAPFK 267

QY 81 HI-----W--IPSSWCSLTEGPECDDTDITATVPYNLRVRATLGSTSAWSILKHPF 131

DB 268 KIPGNHSDKWKQIPN--CENVSTHCVFPREVSSRGYYVVRASNGNGTSFWSSEKEFN 325

QY 132 NNRNSTILTRPGM---BITKDGPHLVI-----ELEDGPQ-----PEFLVAYVRREPGEHV 180

DB 326 TEMKTIIFPPVISKSVTDSDLSHVSVCASESESNMNVNQIPLYEVI FWEINTSNAERKV 385

QY 181 KIVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRY--SAFSQTECVVEVQ-----GEAIPLV 234

DB 386 LEKRTNFI---PPDLKPLTVYCVKARALIENDRRNKGSSFSQDTVCBTKPGNTSKTWLIV 442

QY 235 LALFAFVGFMLILVTVPLFWKMGRLLOYSCCPWWVLPDTLK--ITNSPOK--LISCRRE 290

DB 443 GTCTALFSIPWYIYVVSVEL---RCVKYVFPSPSPSPSSVDYFSDQPLRNLSTSEE 498

QY 291 EVDAC-----ATAVMSPEE 304

DB 499 QTERCFIIENASIITEIEE 517

Search completed: April 5, 2006, 11:40:50

Job time : 113.866 secs

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